

09-774-809

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2003, 07:57:03 / Search time 0.001 Seconds
(without alignments)
58.120 Million cell updates/sec

Title: us-09-774-809-31

Perfect score: 20
Sequence: 1 gtcgggcccagcgaagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 125 seqs, 1453 residues

Total number of hits satisfying chosen parameters: 250

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 171 summaries

Database: rge.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	AR110470
2	20	100.0	20	1	AR116450
3	20	100.0	20	1	AR116461
4	20	100.0	20	1	AX104119
5	20	100.0	20	1	AX164692
6	20	100.0	20	1	AX355435
7	20	100.0	20	1	AX547172
8	20	100.0	20	1	BD074607
9	20	100.0	20	1	BD074618
10	15	75.0	19	1	AX129247
11	14.8	74.0	18	1	AR190756
12	14.4	72.0	17	1	AR188734
13	14	70.0	17	1	AR192173
14	13.4	67.0	17	1	AR145684
15	13.4	67.0	17	1	AR174508
16	13.4	67.0	17	1	AR186508
17	13	65.0	17	1	AR192172
18	12.8	64.0	17	1	AR190307
19	10.4	52.0	12	1	AR167736
20	10.4	52.0	12	1	E29620
21	10.4	52.0	12	1	E38726
22	10.4	52.0	12	1	E64152
23	10	50.0	10	1	AX153495
24	10	50.0	10	1	AX153496
25	9.8	49.0	13	1	AR136587
26	9.8	49.0	13	1	AR285088
27	9.8	49.0	13	1	AR285113
28	9.8	49.0	13	1	BD091222
29	9.4	47.0	11	1	AR301743
30	9.4	47.0	11	1	AX623125
31	9.4	47.0	11	1	AX627385
32	9.4	47.0	11	1	AX630546
33	9.4	47.0	11	1	BD124493

107	8	40.0	10	1	AX153316	ACCESSION:AX153316
108	8	40.0	10	1	AX153317	ACCESSION:AX153317
109	8	40.0	10	1	AX153318	ACCESSION:AX153318
110	8	40.0	10	1	AX153319	ACCESSION:AX153319
111	8	40.0	10	1	BD083124	ACCESSION:BD083124
112	8	40.0	10	1	BD161262	ACCESSION:BD161262
113	8	40.0	10	1	BD167212	ACCESSION:BD167212
114	8	40.0	10	1	E39489	ACCESSION:E39489
115	8	40.0	10	1	E54829	ACCESSION:E54829
116	8	40.0	10	1	AR058606	ACCESSION:AR058606
117	8	40.0	10	1	AR088590	ACCESSION:AR088590
118	8	40.0	10	1	AX152706	ACCESSION:AX152706
119	8	40.0	10	1	AX152961	ACCESSION:AX152961
120	8	40.0	10	1	AX152962	ACCESSION:AX152962
121	8	40.0	10	1	AX153299	ACCESSION:AX153299
122	8	40.0	10	1	AX153300	ACCESSION:AX153300
123	8	40.0	10	1	BD007922	ACCESSION:BD007922
124	8	40.0	10	1	BD007953	ACCESSION:BD007953
125	8	40.0	10	1	BD083213	ACCESSION:BD083213
126	8	40.0	10	1	BD083308	ACCESSION:BD083308
127	8	40.0	10	1	BD161348	ACCESSION:BD161348
128	8	40.0	10	1	BD166572	ACCESSION:BD166572
129	8	40.0	10	1	BD167054	ACCESSION:BD167054
130	8	40.0	10	1	E54715	ACCESSION:E54715
131	7.8	39.0	11	1	AX482038	ACCESSION:AX482038
132	7.8	39.0	11	1	AX511277	ACCESSION:AX511277
133	7.8	39.0	11	1	AX625382	ACCESSION:AX625382
134	7.8	39.0	11	1	AX470751	ACCESSION:AX470751
135	7.8	39.0	11	1	AX629883	ACCESSION:AX629883
136	7.8	39.0	17	1	AR145684	ACCESSION:AR145684
137	7.8	39.0	17	1	AR14508	ACCESSION:AR14508
138	7.6	38.0	20	1	AR110470	ACCESSION:AR110470
139	7.6	38.0	20	1	AR116450	ACCESSION:AR116450
140	7.6	38.0	20	1	AR116461	ACCESSION:AR116461
141	7.6	38.0	20	1	AX104119	ACCESSION:AX104119
142	7.6	38.0	20	1	AX164692	ACCESSION:AX164692
143	7.6	38.0	20	1	AX355435	ACCESSION:AX355435
144	7.6	38.0	20	1	AX547172	ACCESSION:AX547172
145	7.6	38.0	20	1	BD074607	ACCESSION:BD074607
146	7.6	38.0	20	1	BD074618	ACCESSION:BD074618
147	7.4	37.0	9	1	AX205250	ACCESSION:AX205250
148	7.4	37.0	9	1	AX668699	ACCESSION:AX668699
149	7.4	37.0	9	1	AX668700	ACCESSION:AX668700
150	7.4	37.0	10	1	AX224404	ACCESSION:AX224404
151	7.4	37.0	10	1	AX224407	ACCESSION:AX224407
152	7.4	37.0	10	1	AX224410	ACCESSION:AX224410
153	7.4	37.0	10	1	AX153299	ACCESSION:AX153299
154	7.4	37.0	10	1	AX153300	ACCESSION:AX153300
155	7.4	37.0	10	1	BD007953	ACCESSION:BD007953
156	7.4	37.0	11	1	AX625842	ACCESSION:AX625842
157	7.4	37.0	11	1	AX630156	ACCESSION:AX630156
158	7.4	37.0	19	1	AX129247	ACCESSION:AX129247
159	7.4	37.0	9	1	AX017438	ACCESSION:AX017438
160	7.4	37.0	9	1	AX538878	ACCESSION:AX538878
161	7.4	37.0	9	1	AX668947	ACCESSION:AX668947
162	7.4	37.0	9	1	AX668948	ACCESSION:AX668948
163	7.4	37.0	9	1	BD138429	ACCESSION:BD138429
164	7.4	37.0	11	1	AX471339	ACCESSION:AX471339
165	7.4	37.0	11	1	AX623782	ACCESSION:AX623782
166	7.4	37.0	11	1	AX631203	ACCESSION:AX631203
167	6.8	34.0	10	1	AX152961	ACCESSION:AX152961
168	6.8	34.0	10	1	AX152962	ACCESSION:AX152962
169	6.8	34.0	11	1	AX629507	ACCESSION:AX629507
170	6.4	32.0	8	1	E63474	ACCESSION:E63474
171	6.4	32.0	8	1	E63474	ACCESSION:E63474

ALIGNMENTS

RESULT 1
AR110470
LOCUS

AR110470

20 bp

DNA

linear

PAT 14-FEB-2001

DEFINITION Sequence 7 from patent US 6114517.

ACCESSION AR110470

VERSION AR110470.1 GI:12826746

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Montia,B.P. and Xu,X.S.

TITLE

Methods of modulating tumor necrosis factor .alpha.-induced expression of cell adhesion molecules

Patent: US 6114517-A 7 05-SEP-2000;

Location/Qualifiers

1..20

source

BASE COUNT

4 a 7 c 7 g

2 t

Query Match 100.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GTCCGGCCAGGCCAAGTC 20

Db

1 GTCCGGCCAGGCCAAGTC 20

RESULT 2

LOCUS

AR116450 Sequence 31 from patent US 6133246.

ACCESSION

VERSION

AR116450.1 GI:14096772

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS McKay,R., Dean,N., Montia,B.P., Nero,P.S. and Gaarde,W.A.

Antisense oligonucleotide compositions and methods for the

modulation of UNK proteins

Patent: US 6133246-A 31 17-OCT-2000;

Location/Qualifiers

1..20

source

BASE COUNT

4 a 7 c 7 g

2 t

Query Match 100.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GTCCGGCCAGGCCAAGTC 20

Db

1 GTCCGGCCAGGCCAAGTC 20

RESULT 3

LOCUS

AR116461 Sequence 42 from patent US 6133246.

ACCESSION

VERSION

AR116461.1 GI:14096783

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS McKay,R., Dean,N., Montia,B.P., Nero,P.S. and Gaarde,W.A.

Antisense oligonucleotide compositions and methods for the

modulation of UNK proteins

Patent: US 6133246-A 42 17-OCT-2000;

Location/Qualifiers

1..20

source

/organism="unknown"

BASE COUNT 2 a 7 c 7 g 4 t

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCCAAAGTC 20
20 GTCCGGCCAGGCCAAAGTC 1

RESULT 4
AX104119
LOCUS Sequence 311 from Patent WO0122972.
DEFINITION AX104119
ACCESSION AX104119
VERSION AX104119.1 GI:13920316
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Krieger, A.M., Schetter, C. and Vollmer, J.C.
Immunostimulatory nucleic acids
Patent: WO 0122972-A 311 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)

FEATURES
source
1. 20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT 4 a 7 c 7 g 2 t

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCCAAAGTC 20
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RESULT 5
AX164692
LOCUS Sequence 2 from Patent WO0134792.
DEFINITION AX164692
ACCESSION AX164692
VERSION AX164692.1 GI:1454586
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Potapova, O., Gorospe, M. and Holbrook, N.J.
Compositions and methods for the diminution or elimination of
various cancers
Patent: WO 0134792-A 2 17-MAY-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
Location/Qualifiers
1. 20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic"

BASE COUNT 4 a 7 c 7 g 2 t

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCCAAAGTC 20
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DB 1 GTCCGGCCAGGCCAAAGTC 20

RESULT 6
AX355435
LOCUS Sequence 463 from Patent WO0197843.
DEFINITION AX355435
ACCESSION AX355435
VERSION AX355435.1 GI:18620103
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Weiner, G. and Hartmann, G.
Methods for enhancing antibody-induced cell lysis and treating
cancer
Patent: WO 0197843-A 463 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
1. 20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"

FEATURES
source

BASE COUNT 4 a 7 c 7 g 2 t

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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCCAAAGTC 20
|||||

DB 1 GTCCGGCCAGGCCAAAGTC 20

RESULT 7
AX547172
LOCUS Sequence 311 from Patent WO02053141.
DEFINITION AX547172
ACCESSION AX547172
VERSION AX547172.1 GI:25812316
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Bratzler, R.L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 311 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
1. 20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

FEATURES
source

BASE COUNT 4 a 7 c 7 g 2 t

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCCAAAGTC 20
|||||

DB 1 GTCCGGCCAGGCCAAAGTC 20

RESULT 8
BD074607
LOCUS Sequence 20 bp
DEFINITION Antisense oligonucleotide composition and modulation method of JNK

protein.
ACCESSION BD074607 GI:22620210
VERSION BD074607.1
KEYWORDS JP 2001514905-A/31
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Dean,N., Monia,B.P., Scott,P., Nero and Garde,W.A.
TITLE Antisense oligonucleotide composition and modulation method of JNK protein
JOURNAL Patent: JP 2001514905-A 31 18-SEP-2001;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001514905-A/31
PD 18-SEP-2001
PF 07-AUG-1998 JP 2000509875
PI ROBERT MCKAY, NICHOLAS DEAN, BRETT P MONIA, PAMELA SCOTT PI
NERO, WILLIAM A GAARDE
PC C1201/68, A61K31/7088, A61K48/00, A61P35/00, C12N15/09, C12P19/34,
PC C12N15/00
CC antisense sequence
FH Key Location/Qualifiers
FT source 1..20 /organism='Artificial Sequence',
Location/Qualifiers
FEATURES
source 1..20 /organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
BASE COUNT 4 a 7 c 7 g 2 t
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;
QY 1 GTCCGGGCCAGGCCAAAGTC 20
Db 1 GTCCGGGCCAGGCCAAAGTC 20
RESULT 9
BD074618/c
LOCUS
DEFINITION 20 bp DNA linear PAT 27-AUG-2002
ACCESSION BD074618 GI:22620221
VERSION BD074618.1
KEYWORDS JP 2001514905-A/42.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Dean,N., Monia,B.P., Scott,P., Nero and Garde,W.A.
TITLE Antisense oligonucleotide composition and modulation method of JNK protein
JOURNAL Patent: JP 2001514905-A 42 18-SEP-2001;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001514905-A/42
PD 18-SEP-2001
PF 07-AUG-1998 JP 2000509875
PI ROBERT MCKAY, NICHOLAS DEAN, BRETT P MONIA, PAMELA SCOTT PI
NERO, WILLIAM A GAARDE
PC C1201/68, A61K31/7088, A61K48/00, A61P35/00, C12N15/09, C12P19/34,
PC C12N15/00
CC control sequence (sense)
FH Key Location/Qualifiers
FT source 1..20 /organism='Artificial Sequence',
Location/Qualifiers
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source 1..20 /organism='Artificial Sequence',
Location/Qualifiers

source 1..20 /organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
BASE COUNT 2 a 7 c 7 g 4 t
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;
QY 1 GTCCGGGCCAGGCCAAAGTC 20
Db 20 GTCCGGGCCAGGCCAAAGTC 1
RESULT 10
AX129247/c
LOCUS AX129247 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 465 from Patent WO0130362.
ACCESSION AX129247
VERSION AX129247.1 GI:14135552
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Trifcz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 465 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source 1..19 /organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
/note='CDK4 ribozyme binding site'
BASE COUNT 1 a 6 c 7 g 5 t
Query Match 75.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 0; Gaps 0;
QY 6 GGCCAGGCCAAAGTC 20
Db 19 GGCCAGGCCAAAGTC 5
RESULT 11
AR190756/c
LOCUS AR190756 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6244 from patent US 6346398.
ACCESSION AR190756
VERSION AR190756.1 GI:20236721
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSw1ygen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6244 12-FEB-2002;
FEATURES
source 1..18 /organism='unknown'
Location/Qualifiers
BASE COUNT 1 a 6 c 7 g 4 t
Query Match 74.0%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Indels 0; Gaps 0;

QY 3 CCGGGCCAGCCCAAGTC 20
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Db 16 CCGGGCCAGCCCAAGTC 1

RESULT 12
LOCUS AR188734 17 bp DNA
DEFINITION Sequence 4222 from patent US 6346398.
ACCESSION AR188734
VERSION AR188734.1 GI:20234699
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL
FEATURES
source Location/Qualifiers
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/organism="unknown"
BASE COUNT 0 a 5 c 7 g 5 t

Query Match 72.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.6;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGCCCAAG 18
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Db 16 CCGGGCCAGCCCAAG 1

RESULT 13
LOCUS AR192173 17 bp DNA
DEFINITION Sequence 7661 from patent US 6346398.
ACCESSION AR192173
VERSION AR192173.1 GI:20238138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL
FEATURES
source Location/Qualifiers
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/organism="unknown"
BASE COUNT 1 a 5 c 6 g 5 t

Query Match 70.0%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCCAGGCCCAAGTC 20
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Db 17 GCCAGGCCCAAGTC 4

RESULT 14
LOCUS AR145684 17 bp DNA
DEFINITION Sequence 6 from patent US 6218109.
ACCESSION AR145684
VERSION AR145684.1 GI:15108873
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 1 a 5 c 6 g 5 t

REFERENCE 1 (bases 1 to 17)
AUTHORS Elledge,S.J. and Sanchez,Y.
TITLE Mammalian checkpoint genes and proteins
JOURNAL Patent: US 6218109-A 6-17-APR-2001;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 5 a 4 c 5 g 3 t

Query Match 67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.5;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCCAGGCCCAAGTC 20
|||||
Db 3 GCCAGGCCCAAGTC 17

RESULT 15
LOCUS AR174508 17 bp DNA
DEFINITION Sequence 6 from patent US 6307015.
ACCESSION AR174508
VERSION AR174508.1 GI:17914828
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Elledge,S.J. and Sanchez,Y.
TITLE Mammalian checkpoint genes and proteins

JOURNAL
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 5 a 4 c 5 g 3 t

Query Match 67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.5;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCCAGGCCCAAGTC 20
|||||
Db 3 GCCAGGCCCAAGTC 17

RESULT 16
LOCUS AR186508 17 bp DNA
DEFINITION Sequence 1996 from patent US 6346398.
ACCESSION AR186508
VERSION AR186508.1 GI:20232473
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL
FEATURES
source Location/Qualifiers
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/organism="unknown"
BASE COUNT 1 a 5 c 6 g 5 t

Query Match 67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.5;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGCCCAA 17
|||||
Db 15 CCGGGCCAGCCCAA 1

RESULT 17
ARI92172/c 17 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 7660 from patent US 6346398.
DEFINITION ARI92172
ACCESSION ARI92172
VERSION ARI92172.1 GI:20238137
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7660 12-FEB-2002;
FEATURES
source 1..17
/organism="unknown"
BASE COUNT 1 a 4 c 6 g 6 t
Query Match 65.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CCGAGCCCAAGTC 20
17 CCGAGCCCAAGTC 5
Db 17 CCGAGCCCAAGTC 5
RESULT 18
ARI90307/c 17 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 5795 from patent US 6346398.
DEFINITION ARI90307
ACCESSION ARI90307
VERSION ARI90307.1 GI:20236272
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5795 12-FEB-2002;
FEATURES
source 1..17
/organism="unknown"
BASE COUNT 0 a 6 c 7 g 4 t
Query Match 64.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 CCGAGCCCAAGTC 18
16 CCGAGCCCAAGTC 1
Db 16 CCGAGCCCAAGTC 1
RESULT 19
ARI67736 12 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 100 from patent US 6287769.
DEFINITION ARI67736
ACCESSION ARI67736
VERSION ARI67736.1 GI:17903536
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Inoue,T.
TITLE Method of amplifying DNA fragment, apparatus for amplifying DNA

fragment, method of assaying microorganisms, method of analyzing microorganisms and method of assaying contaminant
JOURNAL Patent: US 6287769-A 100 11-SEP-2001;
FEATURES
source 1..12
/organism="unknown"
BASE COUNT 3 a 4 c 4 g 1 t
Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 22;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 CAGGCCCAAGTC 20
1 CAGGCCCAAGTC 12
Db 1 CAGGCCCAAGTC 12
RESULT 20
E29620 12 bp DNA linear PAT 18-JUN-2001
LOCUS Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of waste.
DEFINITION E29620
ACCESSION E29620.1 GI:13021123
VERSION E29620.1 GI:13021123
KEYWORDS JP 1999276176-A/100.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 12)
AUTHORS Koichi,I.
TITLE Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of waste
JOURNAL Patent: JP 1999276176-A 100 12-OCT-1999;
COMMENT SANYO ELECTRIC CO LTD. SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES
OS Unidentified
PN JP 1999276176-A/100
PD 12-OCT-1999
PF 31-MAR-1998 JP 1998087652
PR
PI KOICHI INOUE
PC C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
Strandedness: Single;
FH Key location/Qualifiers
FT source 1..12
/organism="unidentified"
FEATURES
source 1..12
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 3 a 4 c 4 g 1 t
Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 22;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 CAGGCCCAAGTC 20
1 CAGGCCCAAGTC 12
Db 1 CAGGCCCAAGTC 12
RESULT 21
E38726 12 bp DNA linear PAT 31-JAN-2002
LOCUS Method and device for amplifying DNA fragment.
DEFINITION E38726
ACCESSION E38726
VERSION E38726.1 GI:18621388
KEYWORDS JP 2000270867-A/100.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 12)

AUTHORS Inoue,K.
TITLE Method and device for amplifying DNA fragment
JOURNAL Patent: JP 2000270867-A 100 03-OCT-2000;
SANTO ELECTRIC CO. LTD. SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES

COMMENT OS Unidentified
PN JP 2000270867-A/100
PD 03-OCT-2000
PF 19-MAR-1999 JP 1999076844
PR

PI KOICHI INOUE
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source

FEATURES 1.12 Location/Qualifiers
source 1.12 /organism='Unidentified'.
1.12 /organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

BASE COUNT 3 a 4 c 4 g 1 t

Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 22;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CAGGCCAAGTC 20
|||||
1 CAGCCGAGATC 12

Db

RESULT 22
E64152
LOCUS
DEFINITION E64152 12 bp DNA linear PAT 18-JUN-2001
Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method
for analyzing a group of microorganisms, and method for assaying
contaminating substance.

ACCESSION E64152
VERSION E64152.1 GI:13019556
KEYWORDS JP 1999341989-A/100.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kolchi,I.
TITLE Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method for
analyzing a group of microorganisms, and method for assaying
contaminating substance
PATENT: JP 1999341989-A 100 14-DEC-1999;
SANTO ELECTRIC CO LTD. SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES

COMMENT OS Artificial Sequence
PN JP 1999341989-A/100
PD 14-DEC-1999
PF 16-MAR-1999 JP 1999069694
PR

PI KOICHI INOUE
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC
CC Key
FH source

FEATURES 1.12 Location/Qualifiers
source 1.12 /organism='Artificial Sequence'.
1.12 Location/Qualifiers
1.12 /organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

BASE COUNT 3 a 4 c 4 g 1 t

Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 22;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CAGGCCAAGTC 20
|||||
1 CAGCCGAGATC 12

Db

RESULT 23
AX153495/c
LOCUS
DEFINITION AX153495 10 bp DNA linear PAT 22-JUN-2001
Sequence 1410 from Patent WO0138577.
AX153495
ACCESSION AX153495
VERSION AX153495.1 GI:14535146
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

REFERENCE Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
Human transcriptomes
Patent: WO 0138577-A 1411 31-MAY-2001;
The Johns Hopkins University (US)

COMMENT 1.10 Location/Qualifiers
source 1.10 /organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

BASE COUNT 1 a 4 c 4 g 1 t

Query Match 50.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCCGGGCCAG 11
|||||
10 TCCGGGCCAG 1

Db

RESULT 24
AX153496/c
LOCUS
DEFINITION AX153496 10 bp DNA linear PAT 22-JUN-2001
Sequence 1411 from Patent WO0138577.
AX153496
ACCESSION AX153496
VERSION AX153496.1 GI:14535147
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

REFERENCE Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
Human transcriptomes
Patent: WO 0138577-A 1411 31-MAY-2001;
The Johns Hopkins University (US)

COMMENT 1.10 Location/Qualifiers
source 1.10 /organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

BASE COUNT 1 a 4 c 4 g 1 t

Query Match 50.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCCGGGCCAG 11
|||||
10 TCCGGGCCAG 1

Db

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RESULT 25
LOCUS AR136587/c 13 bp DNA PAT 16-JUN-2001
DEFINITION Sequence 77 from patent US 6136952.
ACCESSION AR136587
VERSION AR136587.1 GI:14477259
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Li, L. and Hood, L.
TITLE Human jagged polypeptide, encoding nucleic acids and methods of use
JOURNAL Patent: US 6136952-A 77 24-OCT-2000;
FEATURES
    source 1..13
            /organism="unknown"
BASE COUNT 0 a 4 c 6 g 3 t
Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 35;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGGCCAGGCCAA 17
Db 13 GGGCCAGGCCACA 1

RESULT 26
LOCUS AR285088 13 bp DNA PAT 10-APR-2003
DEFINITION Sequence 11 from patent US 6528268.
ACCESSION AR285088
VERSION AR285088.1 GI:29722005
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Andersson, M.K., Berglund, L.G.T., Reneland, R.H. and Adam, G.I.R.
TITLE Reagents and methods for detection of heart failure
JOURNAL Patent: US 6528268-A 11 04-MAR-2003;
FEATURES
    source 1..13
            Location/Qualifiers
            /organism="unknown"
BASE COUNT 3 a 7 c 3 g 0 t
Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 35;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGGCCAGGCCA 15
Db 1 CCGGCCAGGCCA 13

RESULT 27
LOCUS AR285113/c 13 bp DNA PAT 10-APR-2003
DEFINITION Sequence 36 from patent US 6528268.
ACCESSION AR285113
VERSION AR285113.1 GI:29722030
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Andersson, M.K., Berglund, L.G.T., Reneland, R.H. and Adam, G.I.R.
TITLE Reagents and methods for detection of heart failure
JOURNAL Patent: US 6528268-A 36 04-MAR-2003;
FEATURES
    source 1..13
            Location/Qualifiers
            /organism="unknown"
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BASE COUNT 0 a 3 c 7 g 3 t
Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 35;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGGCCAGGCCA 15
Db 13 CCGGCCAGGCCA 1

RESULT 28
LOCUS BD091222 13 bp DNA PAT 27-AUG-2002
DEFINITION Hetero dimer fused proteins useful against immunotherapy
and general immunostimulation.
ACCESSION BD091222
VERSION BD091222.1 GI:22636832
KEYWORDS JP 2001525423-A/7.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 13)
AUTHORS Gillies, S.D., Lo, K.M. and Lan, Y.
TITLE Hetero dimer fused proteins useful against targeting immunotherapy
JOURNAL Patent: JP 2001525423-A 7 11-DEC-2001;
COMMENT LEXIGEN PHARMACEUTICALS CORP
OS Artificial Sequence
PN JP 2001525423-A/7
PD 11-DEC-2001
PF 08-DEC-1998 JP 2000524321
PR 08-DEC-1997 US 08/986997
PI STEPHEN D GILLIES, KIN MING LO, YAN LAN
PC C07K19/00, A61K47/48, A61P37/04, C07K14/54, C07K16/30, C12N15/09,
PC C12P21/00, A61K38/00, C12N15/00, A61K37/02
PC A61K38/00
CC Description of Artificial Sequence: Synthetic Oligonucleotide
FH Key
FT source 1..13
    Location/Qualifiers
    /organism="Artificial Sequence"
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
BASE COUNT 3 a 5 c 4 g 1 t
Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 35;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGGCCAGGCCA 15
Db 1 CCGGCCAGGCCA 13

RESULT 29
LOCUS AR301743 11 bp DNA PAT 12-JUN-2003
DEFINITION Sequence 324 from patent US 6538173.
ACCESSION AR301743
VERSION AR301743.1 GI:31689545
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz, E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 324 25-MAR-2003;
FEATURES
    source 1..11
            Location/Qualifiers
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Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCCGGCGCAGG 12
 |||||
 Db 1 TCCGGCGCAGG 11

RESULT 34
 AX482038/c 11 bp DNA linear PAT 16-AUG-2002
 LOCUS Sequence 15 from Patent EP1225233.
 DEFINITION AX482038
 ACCESSION AX482038 GI:22316760
 VERSION
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS van der Kuy1,A.C. and Cornelissen,M.
 TITLE Means and methods for treatment evaluation
 JOURNAL Patent: EP 1225233-A 15 24-JUL-2002;
 Amsterdam Support Diagnostics B.V. (NL)
 Location/Qualifiers
 1..11
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="TAG sequence Hs74649 and Hs288761"

BASE COUNT 1 a 5 c 4 g 1 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGCC 14
 |||||
 Db 11 GGCCAGGCC 3

RESULT 35
 AX511277/c 11 bp DNA linear PAT 28-SEP-2002
 LOCUS Sequence 15 from Patent WO02059558.
 DEFINITION AX511277
 ACCESSION AX511277
 VERSION AX511277.1 GI:23392154
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS van der Kuy1,A.C. and Cornelissen,M.
 TITLE Means and methods for treatment evaluation
 JOURNAL Patent: WO 02059558-A 15 01-AUG-2002;
 Amsterdam Support Diagnostics B.V. (NL)
 Location/Qualifiers
 1..11
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="TAG sequence Hs74649 and Hs288761"

BASE COUNT 1 a 5 c 4 g 1 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGCC 14
 |||||
 Db 11 GGCCAGGCC 3

RESULT 36
 AX623635/c

LOCUS AX623635 11 bp DNA linear PAT 21-FEB-2003
 DEFINITION Sequence 676 from Patent WO02053774.
 ACCESSION AX623635
 VERSION AX623635.1 GI:28451576
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 676 11-JUL-2002;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 Location/Qualifiers
 1..11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 2 c 3 g 5 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CAGGCCCAA 17
 |||||
 Db 10 CAGGCCCAA 2

RESULT 37
 AX625164/c 11 bp DNA linear PAT 21-FEB-2003
 LOCUS Sequence 2205 from Patent WO02053774.
 DEFINITION AX625164
 ACCESSION AX625164
 VERSION AX625164.1 GI:28453105
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 2205 11-JUL-2002;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 Location/Qualifiers
 1..11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 2 c 4 g 4 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCAA 16
 |||||
 Db 11 CCAGGCCAA 3

RESULT 38
 AX625382/c 11 bp DNA linear PAT 21-FEB-2003
 LOCUS Sequence 2423 from Patent WO02053774.
 DEFINITION AX625382
 ACCESSION AX625382
 VERSION AX625382.1 GI:28453123
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 2423 11-JUL-2002;
 FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
 source Location/Qualifiers
 1. 11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 5 c 4 g 1 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGCC 14
 11 GGCCAGGCC 3

RESULT 39
 AX629145/c 11 bp DNA linear PAT 21-FEB-2003
 LOCUS Sequence 6186 from Patent WO02053774.
 DEFINITION AX629145
 ACCESSION AX629145
 VERSION AX629145.1 GI:28457183
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 6186 11-JUL-2002;
 FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
 source Location/Qualifiers
 1. 11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 0 a 3 c 5 g 3 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCAA 16
 11 CCAGGCCAA 3

RESULT 40
 AX629339/c 11 bp DNA linear PAT 21-FEB-2003
 LOCUS Sequence 6380 from Patent WO02053774.
 DEFINITION AX629339
 ACCESSION AX629339
 VERSION AX629339.1 GI:28457377
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 6380 11-JUL-2002;
 FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
 source Location/Qualifiers
 1. 11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"

BASE COUNT 1 a 2 c 4 g 4 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCAA 16
 11 CCAGGCCAA 3

RESULT 42
 AX632585/c 11 bp DNA linear PAT 21-FEB-2003
 LOCUS Sequence 9627 from Patent WO02053774.
 DEFINITION AX632585
 ACCESSION AX632585
 VERSION AX632585.1 GI:28468200
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 9627 11-JUL-2002;
 FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
 source Location/Qualifiers
 1. 11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"

BASE COUNT 0 a 2 c 5 g 4 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCAA 16
 10 CCAGGCCAA 2

RESULT 41
 AX631056/c 11 bp DNA linear PAT 21-FEB-2003
 LOCUS Sequence 8097 from Patent WO02053774.
 DEFINITION AX631056
 ACCESSION AX631056
 VERSION AX631056.1 GI:28459098
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 8097 11-JUL-2002;
 FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
 source Location/Qualifiers
 1. 11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 2 c 3 g 5 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CAGGCCAAA 17
 10 CAGGCCAAA 2

RESULT 42
 AX632585/c 11 bp DNA linear PAT 21-FEB-2003
 LOCUS Sequence 9627 from Patent WO02053774.
 DEFINITION AX632585
 ACCESSION AX632585
 VERSION AX632585.1 GI:28468200
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 9627 11-JUL-2002;
 FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
 source Location/Qualifiers
 1. 11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 2 c 4 g 4 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCAA 16
 11 CCAGGCCAA 3

RESULT 40
 AX629339/c 11 bp DNA linear PAT 21-FEB-2003
 LOCUS Sequence 6380 from Patent WO02053774.
 DEFINITION AX629339
 ACCESSION AX629339
 VERSION AX629339.1 GI:28457377
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 6380 11-JUL-2002;
 FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
 source Location/Qualifiers
 1. 11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"

BASE COUNT 1 a 2 c 4 g 4 t

Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 CCAGGCCAA 3

RESULT 43
LOCUS AR107817/c 10 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 63 from patent US 6110667.
ACCESSION AR107817
VERSION AR107817.1 GI:12823304
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo, and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 63/29-AUG-2000;
FEATURES
source Location/Qualifiers
1..10
/organism="unknown"

BASE COUNT 0 a 4 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGGGCCAGGC 13
10 CGGGCCAGGC 1

Db 10 CGGGCCAGGC 1

RESULT 44
LOCUS AX152505/c 10 bp DNA PAT 22-JUN-2001
DEFINITION Sequence 420 from Patent W00138577.
ACCESSION AX152505
VERSION AX152505.1 GI:14534156
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcripts
JOURNAL Patent: WO 0138577-A 420 31-MAY-2001;
FEATURES
source Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 0 a 5 c 3 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGGCAGGCCA 15
10 GGGCAGGCCA 1

Db 10 GGGCAGGCCA 1

RESULT 45
LOCUS AX152506/c 10 bp DNA PAT 22-JUN-2001
DEFINITION Sequence 421 from Patent W00138577.
ACCESSION AX152506
VERSION AX152506.1 GI:14534157
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcripts
JOURNAL Patent: WO 0138577-A 421 31-MAY-2001;
FEATURES
source Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 0 a 5 c 3 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGGCAGGCCA 15
10 GGGCAGGCCA 1

Db 10 GGGCAGGCCA 1

RESULT 46
LOCUS AX152507 10 bp DNA PAT 22-JUN-2001
DEFINITION Sequence 422 from Patent W00138577.
ACCESSION AX152507
VERSION AX152507.1 GI:14534158
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcripts
JOURNAL Patent: WO 0138577-A 422 31-MAY-2001;
FEATURES
source Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 3 a 3 c 4 g 0 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GGGCAAGTC 20
1 GGGCAAGTC 10

Db 1 GGGCAAGTC 10

RESULT 47
LOCUS AX152729 10 bp DNA PAT 22-JUN-2001
DEFINITION Sequence 644 from Patent W00138577.
ACCESSION AX152729
VERSION AX152729.1 GI:14534380
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcripts
JOURNAL Patent: WO 0138577-A 644 31-MAY-2001;
FEATURES
source Location/Qualifiers
1..10

BASE COUNT 5 a 2 c 2 g 1 t
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 51;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 10 AGGCCAAAGT 19
 |||||
 1 AGACCAAGT 10

RESULT 48
 AX153313/c 10 bp DNA linear PAT 22-JUN-2001
 LOCUS Sequence 1228 from Patent WO0138577.
 DEFINITION AX153313
 ACCESSION AX153313
 VERSION AX153313.1 GI:14534964
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 1228 31-MAY-2001;
 The Johns Hopkins University (US)
 Location/Qualifiers

FEATURES
 source 1..10
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 3 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 51;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7 GCCAGGCCAA 16
 |||||
 10 GCCTGGCCAA 1

RESULT 49
 AX153314/c 10 bp DNA linear PAT 22-JUN-2001
 LOCUS Sequence 1229 from Patent WO0138577.
 DEFINITION AX153314
 ACCESSION AX153314
 VERSION AX153314.1 GI:14534965
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 1229 31-MAY-2001;
 The Johns Hopkins University (US)
 Location/Qualifiers

FEATURES
 source 1..10
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 3 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 51;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7 GCCAGGCCAA 16
 |||||
 10 GCCTGGCCAA 1

RESULT 50
 AX153315/c 10 bp DNA linear PAT 22-JUN-2001
 LOCUS Sequence 1230 from Patent WO0138577.
 DEFINITION AX153315
 ACCESSION AX153315
 VERSION AX153315.1 GI:14534966
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 1230 31-MAY-2001;
 The Johns Hopkins University (US)
 Location/Qualifiers

FEATURES
 source 1..10
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 3 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 51;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7 GCCAGGCCAA 16
 |||||
 10 GCCTGGCCAA 1

RESULT 51
 AX153316/c 10 bp DNA linear PAT 22-JUN-2001
 LOCUS Sequence 1231 from Patent WO0138577.
 DEFINITION AX153316
 ACCESSION AX153316
 VERSION AX153316.1 GI:14534967
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 1231 31-MAY-2001;
 The Johns Hopkins University (US)
 Location/Qualifiers

FEATURES
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 3 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 51;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7 GCCAGGCCAA 16
 |||||
 10 GCCTGGCCAA 1

RESULT 52
 AX153317/c 10 bp DNA linear PAT 22-JUN-2001
 LOCUS Sequence 1232 from Patent WO0138577.

ACCESSION AX153317
VERSION AX153317.1 GI:14534968
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Human transcriptomes
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1234 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1.10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 3 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
10 GCCTGGCCAA 1

RESULT 53
AX153318/c
LOCUS AX153318
DEFINITION Sequence 1233 from Patent W00138577.
ACCESSION AX153318
VERSION AX153318.1 GI:14534969
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Human transcriptomes
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1233 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1.10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 3 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
10 GCCTGGCCAA 1

RESULT 54
AX153319/c
LOCUS AX153319
DEFINITION Sequence 1234 from Patent W00138577.
ACCESSION AX153319
VERSION AX153319.1 GI:14534970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Human transcriptomes
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1234 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1.10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 3 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
10 GCCTGGCCAA 1

RESULT 55
AX224404/c
LOCUS AX224404
DEFINITION Sequence 11 from Patent W00160997.
ACCESSION AX224404
VERSION AX224404.1 GI:15554646
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Albertsen, M.C., Fox, T.W., Garnat, C.W., Huffman, G. and Kendall, T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1.10
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
BASE COUNT 0 a 5 c 5 g 0 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGGGCCGGC 13
10 CGGGCCGGC 1

RESULT 56
AX224407
LOCUS AX224407
DEFINITION Sequence 14 from Patent W00160997.
ACCESSION AX224407
VERSION AX224407.1 GI:15554649
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Albertsen, M.C., Fox, T.W., Garnat, C.W., Huffman, G. and Kendall, T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1.10
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"

TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1234 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1.10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 3 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
10 GCCTGGCCAA 1

RESULT 55
AX224404/c
LOCUS AX224404
DEFINITION Sequence 11 from Patent W00160997.
ACCESSION AX224404
VERSION AX224404.1 GI:15554646
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Albertsen, M.C., Fox, T.W., Garnat, C.W., Huffman, G. and Kendall, T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1.10
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
BASE COUNT 0 a 5 c 5 g 0 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGGGCCGGC 13
10 CGGGCCGGC 1

RESULT 56
AX224407
LOCUS AX224407
DEFINITION Sequence 14 from Patent W00160997.
ACCESSION AX224407
VERSION AX224407.1 GI:15554649
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Albertsen, M.C., Fox, T.W., Garnat, C.W., Huffman, G. and Kendall, T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1.10
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"

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BASE COUNT      0 a _db_xref="taxon:4577"      5 g      0 t
Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGGCCAGGC 13
    |||||
    1 CGGCCCGGC 10

RESULT 57
AX224410/c      10 bp      DNA      linear      PAT 10-SEP-2001
LOCUS
DEFINITION      Sequence 17 from Patent WO0160997.
ACCESSION
VERSION          AX224410
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS          Albertsen,M.C., Fox,T.W., Garnat,C.W., Huffman,G. and Kendall,T.L.
TITLE            Male tissue-preferred regulatory region and method of using same
JOURNAL          Patent: WO 0160997-A 17 23-AUG-2001;
                  PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
  1..10
  /organism="Zea mays"
  /mol_type="genomic DNA"
  /db_xref="taxon:4577"

BASE COUNT      0 a      5 c      5 g      0 t
Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGCC 14
    |||||
    10 GGGCCCGGC 1

RESULT 58
AX301480/c      10 bp      DNA      linear      PAT 30-NOV-2001
LOCUS
DEFINITION      Sequence 194 from Patent WO0185941.
ACCESSION
VERSION          AX301480
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS          Versteg,R. and Caron,H.N.
TITLE            MYC targets
JOURNAL          Patent: WO 0185941-A 194 15-NOV-2001;
                  Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES
source
  1..10
  /organism="Homo sapiens"
  /mol_type="genomic DNA"
  /db_xref="taxon:9606"

BASE COUNT      0 a      5 c      3 g      2 t
Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGGCAGGCCA 15

```

```

Db 10 GGGCAGGCCA 1
    |||||
    10 GGGCAGGCCA 1

RESULT 59
BD007979/c      10 bp      DNA      linear      PAT 31-JAN-2002
LOCUS
DEFINITION      LPS activated human monocyte expressing genes.
ACCESSION
VERSION          BD007979
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS          Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE            LPS activated human monocyte expressing genes
JOURNAL          Patent: JP 2001069993-A 255 21-MAR-2001;
                  JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT
OS              Homo sapiens (human)
PN              JP 2001069993-A/255
PD              21-MAR-2001
PF              28-Apr-2000 JP 2000131079
PR
PI              KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC              A61P31/00,C12P21/08,C12N15/00
CC
FH              Key
FT              source
FT              Location/Qualifiers
  1..10
  /organism="Homo sapiens"
  /mol_type="genomic DNA"
  /db_xref="taxon:9606"

BASE COUNT      1 a      4 c      4 g      1 t
Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGCC 14
    |||||
    10 GTGCCAGGCC 1

RESULT 60
BD065145/c      10 bp      DNA      linear      PAT 27-AUG-2002
LOCUS
DEFINITION      Characterization of the yeast transcriptome.
ACCESSION
VERSION          BD065145
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS          Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE            Characterization of the yeast transcriptome
JOURNAL          Patent: JP 2001509017-A 81 10-JUL-2001;
                  THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT
OS              Saccharomyces cerevisiae (Yeast)
PN              JP 2001509017-A/81
PD              10-JUL-2001
PF              22-JAN-1998 JP 1998532117
PR              23-JAN-1997 US 60/035917
PI              VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10 C12N15/31,C07K14/395,C1201/68,C1201/02 CC
Characterization of the yeast transcriptome

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FEATURES
source
FH Key Location/Qualifiers
FT source 1..10 /organism="Saccharomyces cerevisiae (yeast)"
FT /db_xref="taxon:4932"

BASE COUNT
0 a 5 c 3 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCAGGCCA 15
DB 10 GGCAGGCCA 1

RESULT 61
BD083124/c 10 bp DNA linear PAT 27-AUG-2002
LOCUS Human matured/activated dendritic cell expression genes.
DEFINITION BD083124
ACCESSION BD083124.1 GI:22628734
VERSION JP 2001327293-A/45.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 10)
REFERENCE Matushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 45 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/45
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
COMMENT FH Key Location/Qualifiers
1..10 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT
1 a 3 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
DB 10 GCCTGGCCAA 1

RESULT 62
BD161262/c 10 bp DNA linear PAT 17-JAN-2003
LOCUS Human activated Th1 and Th2 cell expression genes.
DEFINITION BD161262
ACCESSION BD161262.1 GI:27867020
VERSION JP 2002186482-A/84.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 10)
REFERENCE Nagai,S., Matushima,K. and Hashimoto,S.
AUTHORS

TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 84 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/84
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers 1..10
FT source /organism="Homo sapiens (human)"
FT source 1..10 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT
1 a 3 c 4 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
DB 10 GCCTGGCCAA 1

RESULT 63
BD166487 10 bp DNA linear PAT 17-JAN-2003
LOCUS Human liver disease-expressing genes.
DEFINITION BD166487
ACCESSION BD166487.1 GI:27872299
VERSION JP 2002209591-A/32.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified.
1 (bases 1 to 10)
REFERENCE Matushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
AUTHORS Human liver disease-expressing genes.
TITLE Patent: JP 2002209591-A 32 30-JUL-2002;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/32
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10 Location/Qualifiers
/organism="Homo sapiens (human)"
FT source 1..10 Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT
5 a 2 c 2 g 1 t

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AGCCAAACT 19
DB 1 AGCCAAACT 10

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RESULT 64
BD166906/c
LOCUS      BD166906      10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166906
VERSION    BD166906.1 GI:27872718
KEYWORDS   JP 2002209591-A/451.
SOURCE     unidentified
ORGANISM   unclassified

REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE     Human liver disease-expressing genes
JOURNAL   Patent: JP 2002209591-A 451 30-JUL-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT    OS Homo sapiens (human)
           PN JP 2002209591-A/451
           PD 30-JUL-2002
           PF 19-JAN-2001 JP 2001012328
           PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
           YAMASHITA
           PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
           PC C12P21/08,
           PC C12N15/00
           CC Human liver disease-expressing genes
           FH Key
           FT source
           FT source

FEATURES
source
1..10
/organism="unclassified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT  1 a      2 c      3 g      4 t

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 AGGCCAAAGT 19
Db 10 AGGCCAAACT 1

RESULT 65
BD167212/c
LOCUS      BD167212      10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167212
VERSION    BD167212.1 GI:27873024
KEYWORDS   JP 2002209591-A/757.
SOURCE     unidentified
ORGANISM   unclassified

REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE     Human liver disease-expressing genes
JOURNAL   Patent: JP 2002209591-A 757 30-JUL-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP
          OS Homo sapiens (human)
          PN JP 2002209591-A/757
          PD 30-JUL-2002
          PF 19-JAN-2001 JP 2001012328
          PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
          YAMASHITA
          PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
          PC C12P21/08,
          PC C12N15/00
          CC Human liver disease-expressing genes
          FH Key
          FT source
          FT source

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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT  1 a      3 c      4 g      2 t

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Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCCAA 16
Db 10 GCCTGGCCAA 1

RESULT 66
E39489
LOCUS      E39489      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION  E39489
VERSION    E39489.1 GI:18621580
KEYWORDS   JP 2000279181-A/22.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE  1 (bases 1 to 10)
AUTHORS   Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE     Genes with human dendritic cell expression
JOURNAL   Patent: JP 2000279181-A 22 10-OCT-2000;
          SCIENCE & TECH AGENCY
          OS Homo sapiens (human)
          PN JP 2000279181-A/22
          PD 10-OCT-2000
          PF 01-APR-1999 JP 1999095481
          PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
          PI C12N15/09,C07K14/475,C07K16/18,C12N15/00
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          FH Key
          FT source
          FT source

FEATURES
Location/Qualifiers
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT  1 a      3 c      4 g      2 t

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCCAA 16
Db 10 GCCTGGCCAA 1

RESULT 67
E39743
LOCUS      E39743      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION  E39743
VERSION    E39743.1 GI:18621834
KEYWORDS   JP 2000279181-A/276.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE  1 (bases 1 to 10)
AUTHORS   Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE     Genes with human dendritic cell expression
JOURNAL   Patent: JP 2000279181-A 276 10-OCT-2000;
          SCIENCE & TECH AGENCY
          OS Homo sapiens (human)
          PN JP 2000279181-A/276
          PD 10-OCT-2000
          PF 01-APR-1999 JP 1999095481
          PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
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Location/Qualifiers
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Location/Qualifiers
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COMMENT      SCIENCE & TECH AGENCY
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PN           JP 2000279181-A/276
PD           10-OCT-2000
PF           01-APR-1999 JP 1999095481
PR           SHINICHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI PC
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CC           Key
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              1 t

BASE COUNT   1 a
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              4 g
              1 t

Query Match   42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY           5 GGGCCAGGCC 14
Db           10 GTCCAGGCC 1

RESULT 68
E54829/c     10 bp   DNA
DEFINITION   Human normal liver cell expression genes.
ACCESSION    E54829
VERSION      E54829.1 GI:22556312
KEYWORDS     JP 2001211883-A/181.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
TITLE        Human normal liver cell expression genes
JOURNAL      Patent: JP 2001211883-A 181 07-AUG-2001;
SCIENCE & TECH AGENCY
OS           Homo sapiens (human)
PN           JP 2001211883-A/181
PD           07-AUG-2001
PF           31-JAN-2000 JP 2000023170
PR           KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC           C12N15/09, C07K16/18, C12P21/02, C12N15/00
CC           Key
FH           Location/Qualifiers
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              /mol_type="genomic DNA"
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              4 g
              2 t

BASE COUNT   1 a
              3 c
              4 g
              2 t

Query Match   42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY           7 GCCAGGCCAA 16
Db           10 GCCTGGCCAA 1

RESULT 69
AX623125     11 bp   DNA
DEFINITION   Sequence 166 from Patent WO02053774.

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ACCESSION    AX623125
VERSION      AX623125.1 GI:28451066
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conradt, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 166 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
              Location/Qualifiers
              source
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                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                4 c
                5 g
                1 t

BASE COUNT   1 a
              4 c
              5 g
              1 t

Query Match   42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY           3 CCGGCCAGG 12
Db           2 CCGGCCAGG 11

RESULT 70
AX630546     11 bp   DNA
DEFINITION   Sequence 7587 from Patent WO02053774.
ACCESSION    AX630546
VERSION      AX630546.1 GI:28458584
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conradt, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7587 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
              Location/Qualifiers
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BASE COUNT   1 a
              4 c
                5 g
                1 t

Query Match   42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY           3 CCGGCCAGG 12
Db           2 CCGGCCAGG 11

RESULT 71
AX393189     11 bp   DNA
DEFINITION   Sequence 119 from Patent WO0210217.
ACCESSION    AX393189
VERSION      AX393189.1 GI:19701239
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1
AUTHORS      St Croix, B., Kinzler, K.W. and Vogelstein, B.

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TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 119 07-FEB-2002;
The Johns Hopkins University (US).

FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 4 a 3 c 3 g 1 t

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AGGCCCAAGT 19
Db 1 AGGCCCAAGT 10

RESULT 72
AX470637 11 bp DNA linear PAT 09-AUG-2002
LOCUS Sequence 214 from Patent WO02053773.
DEFINITION AX470637
ACCESSION AX470637
VERSION AX470637.1 GI:22205762
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 214 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 3 a 3 c 3 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AGGCCCAAGT 19
Db 2 AGGCCCAAGT 11

RESULT 73
AX470751 11 bp DNA linear PAT 09-AUG-2002
LOCUS Sequence 328 from Patent WO02053773.
DEFINITION AX470751
ACCESSION AX470751
VERSION AX470751.1 GI:22205876
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 328 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 0 a 4 c 5 g 2 t

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
Db 11 GCCAGGCCCA 2

RESULT 74
AX471339 11 bp DNA linear PAT 09-AUG-2002
LOCUS Sequence 916 from Patent WO02053773.
DEFINITION AX471339
ACCESSION AX471339
VERSION AX471339.1 GI:22206464
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 916 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 4 a 4 c 2 g 1 t

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCAGGCCCAA 17
Db 1 CCTGGCCCAA 10

RESULT 75
AX471385 11 bp DNA linear PAT 09-AUG-2002
LOCUS Sequence 962 from Patent WO02053773.
DEFINITION AX471385
ACCESSION AX471385
VERSION AX471385.1 GI:22206510
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 962 11-JUL-2002;
HENKEL KGAA (DE)
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 5 a 2 c 3 g 1 t

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AGGCCCAAGT 19
Db 1 AGGCCCAAGT 10

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RESULT 76
LOCUS AX482027 11 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 4 from Patent EP1225233.
ACCESSION AX482027
VERSION AX482027.1 GI:22316749
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 van der Kuyl,A.C. and Cornelissen,M.
AUTHORS Means and methods for treatment evaluation
TITLE Patent: EP 1225233-A 4 24-JUL-2002;
JOURNAL Amsterdam Support Diagnostics B.V. (NL)
FEATURES
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1. .11
Location/Qualifiers
/mol_type="synthetic construct"
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/note="TAG sequence Hs78436"
BASE COUNT 3 a 4 c 4 g 0 t
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 GGCCAAAGTC 20
Db 1 GGCCAAAGGC 10

RESULT 77
LOCUS AX511266 11 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 4 from Patent WO02059558.
ACCESSION AX511266
VERSION AX511266.1 GI:23392143
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 van der Kuyl,A.C. and Cornelissen,M.
AUTHORS Means and methods for treatment evaluation
TITLE Patent: WO 02059558-A 4 01-AUG-2002;
JOURNAL Amsterdam Support Diagnostics B.V. (NL)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="TAG sequence Hs78436"
BASE COUNT 3 a 4 c 4 g 0 t
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 GGCCAAAGTC 20
Db 1 GGCCAAAGGC 10

RESULT 78
LOCUS AX623296/c 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 337 from Patent WO02053774.
ACCESSION AX623296
VERSION AX623296.1 GI:28451237
KEYWORDS
SOURCE
Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 337 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
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Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 1 a 4 c 4 g 2 t
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GGCCGAGGCC 14
Db 10 GTGCCAGGCC 1

RESULT 79
LOCUS AX623449 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 490 from Patent WO02053774.
ACCESSION AX623449
VERSION AX623449.1 GI:28451390
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 490 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 1 a 5 c 4 g 1 t
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GGCCGAGGCC 14
Db 1 GGCCGAGGCC 10

RESULT 80
LOCUS AX623782 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 823 from Patent WO02053774.
ACCESSION AX623782
VERSION AX623782.1 GI:28451723
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 823 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers

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BASE COUNT	4 a	4 c	2 g	1 t
Query Match	42.0%	Score 8.4;	DB 1;	Length 11;
Best Local Similarity	90.0%	Pred. No. 58;		
Matches	9;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	8	CCAGGCCAAA	17	
DB	1	CTGGCCAAA	10	
RESULT 81				
LOCUS	AX625842		11 bp	DNA
DEFINITION	Sequence 2883 from Patent WO02053774.			linear
ACCESSION	AX625842			
VERSION	AX625842.1			
KEYWORDS	GI:28453878			
SOURCE				
ORGANISM	Homo sapiens (human)			
REFERENCE				
AUTHORS	Petersohn, D., Conradt, M., and Hofmann, K.			
TITLE	Method for determining homeostasis of the skin			
JOURNAL	Patent: WO 02053774-A 2883 11-JUL-2002;			
FEATURES	Henkel Kommanditgesellschaft auf Aktien (DE)			
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	/mol_type="genomic DNA"			
	/db_xref="taxon:9606"			
BASE COUNT	2 a	4 c	5 g	0 t
Query Match	42.0%	Score 8.4;	DB 1;	Length 11;
Best Local Similarity	90.0%	Pred. No. 58;		
Matches	9;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	4	CGGCGCAGGC	13	
DB	1	CTGGCCAGGC	10	
RESULT 82				
LOCUS	AX625891		11 bp	DNA
DEFINITION	Sequence 2932 from Patent WO02053774.			linear
ACCESSION	AX625891			
VERSION	AX625891.1			
KEYWORDS	GI:28453929			
SOURCE				
ORGANISM	Homo sapiens (human)			
REFERENCE				
AUTHORS	Petersohn, D., Conradt, M., and Hofmann, K.			
TITLE	Method for determining homeostasis of the skin			
JOURNAL	Patent: WO 02053774-A 2932 11-JUL-2002;			
FEATURES	Henkel Kommanditgesellschaft auf Aktien (DE)			
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	/db_xref="taxon:9606"			
BASE COUNT	2 a	4 c	5 g	0 t

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DEFINITION Sequence 3928 from Patent WO02053774.
ACCESSION AX626887
VERSION AX626887.1 GI:28454925
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3928 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GGCCAAAGTC 20
Db 10 GGCCAGAGTC 1

RESULT 86
AX627709/c 11 bp DNA linear PAT 21-FEB-2003
LOCUS AX627709
DEFINITION Sequence 4750 from Patent WO02053774.
ACCESSION AX627709
VERSION AX627709.1 GI:28455747
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4750 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
Db 10 GCCCGGCCAA 1

RESULT 87
AX628172/c 11 bp DNA linear PAT 21-FEB-2003
LOCUS AX628172
DEFINITION Sequence 5213 from Patent WO02053774.
ACCESSION AX628172
VERSION AX628172.1 GI:28456210
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5213 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

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AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5213 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/db_xref="taxon:9606"
BASE COUNT 1 a 4 c 5 g 1 t
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGCCAGGCC 14
Db 11 GGCCAGGCC 2

RESULT 88
AX628292 11 bp DNA linear PAT 21-FEB-2003
LOCUS AX628292
DEFINITION Sequence 5333 from Patent WO02053774.
ACCESSION AX628292
VERSION AX628292.1 GI:28456330
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5333 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1..11
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 3 c 3 g 2 t
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AGGCCAAAGT 19
Db 2 AGGCCCAAGT 11

RESULT 89
AX629263/c 11 bp DNA linear PAT 21-FEB-2003
LOCUS AX629263
DEFINITION Sequence 6304 from Patent WO02053774.
ACCESSION AX629263
VERSION AX629263.1 GI:28457301
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6304 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1..11
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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BASE COUNT      1 a      5 c      4 g      1 t
Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TCCGGGCCAG 11
        |||||||
Db      10 TCCGGGCCAG 1

RESULT 90
AX629507/c
LOCUS      AX629507
DEFINITION Sequence 6548 from Patent WO02053774.
ACCESSION  AX629507
VERSION     AX629507.1 GI:28457545
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 6548 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            1..11
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"

BASE COUNT      1 a      5 c      3 g      2 t
Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GCCCAGGCCA 15
        |||||||
Db      10 GCCCAGGCCA 1

RESULT 91
AX629798
LOCUS      AX629798
DEFINITION Sequence 6839 from Patent WO02053774.
ACCESSION  AX629798
VERSION     AX629798.1 GI:28457836
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 6839 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            1..11
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"

BASE COUNT      3 a      4 c      4 g      0 t
Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 GCCCAAGTC 20
        |||||||
Db      1 GCCCAAGTC 10
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```
RESULT 92
AX629883/c
LOCUS      AX629883
DEFINITION Sequence 6924 from Patent WO02053774.
ACCESSION  AX629883
VERSION     AX629883.1 GI:28457921
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 6924 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            1..11
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"

BASE COUNT      0 a      4 c      5 g      2 t
Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCCCAGGCCA 16
        |||||||
Db      11 GCCCAGGCCA 2

RESULT 93
AX630156/c
LOCUS      AX630156
DEFINITION Sequence 7197 from Patent WO02053774.
ACCESSION  AX630156
VERSION     AX630156.1 GI:28458194
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 7197 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            1..11
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"

BASE COUNT      0 a      3 c      5 g      3 t
Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCCCAGGCCA 16
        |||||||
Db      10 GCCCAGGCCA 1

RESULT 94
AX630273/c
LOCUS      AX630273
DEFINITION Sequence 7314 from Patent WO02053774.
ACCESSION  AX630273
VERSION     AX630273.1 GI:28458311
KEYWORDS
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7314 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    source
            1..11
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

BASE COUNT      2 a      4 c      4 g      1 t

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              5 GGGCCAGGCC 14
                |||||
                10 GGGCCAGCTCC 1

RESULT 95
AX630717/c      AX630717      11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS           Sequence 7758 from Patent WO02053774.
DEFINITION      AX630717
ACCESSION       AX630717.1 GI:28458755
VERSION         AX630717.1 GI:28458755
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7758 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    source
            1..11
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

BASE COUNT      1 a      4 c      4 g      2 t

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              5 GGGCCAGGCC 14
                |||||
                10 GGGCCAGGCC 1

RESULT 96
AX630870
LOCUS           Sequence 7911 from Patent WO02053774.
DEFINITION      AX630870
ACCESSION       AX630870.1 GI:28458910
VERSION         AX630870.1 GI:28458910
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7911 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)

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FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

BASE COUNT      1 a      5 c      4 g      1 t

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              5 GGGCCAGGCC 14
                |||||
                1 GGGCCAGGCC 10

RESULT 97
AX631203
LOCUS           AX631203      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION      Sequence 8245 from Patent WO02053774.
ACCESSION       AX631203
VERSION         AX631203.1 GI:28459249
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8245 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    source
            1..11
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

BASE COUNT      4 a      4 c      2 g      1 t

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              8 CCAGGCCAAA 17
                |||||
                1 CCGGCCAAA 10

RESULT 98
BD135851
LOCUS           BD135851      11 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION      Selective regulation of adenovirus production.
ACCESSION       BD135851
VERSION         BD135851.1 GI:23230796
KEYWORDS        JP 2002506355-A/22.
SOURCE          unidentified adenovirus
ORGANISM        unidentified adenovirus
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

REFERENCE   1 (bases 1 to 11)
AUTHORS     Hearing,P., Schmid,S.I., Ostapchuk,P.H. and Erturk,E.
TITLE       Selective regulation of adenovirus production
JOURNAL     Patent: JP 2002506355-A 22 26-FEB-2002;
            THE RESEARCH FOUNDATION OF STATE UNIVERSITY OF NEW YORK
COMMENT      OS Adenovirus
            PN JP 2002506355-A/22
            PD 26-FEB-2002
            PF 15-APR-1999 JP 1999552110
            PR 15-APR-1998 US 60/081867,05-JUN-1998 US 60/088321 PI
            PATRICK HEARING,SUSANNE I SCHMID,PHILONINA H OSTAPCHUK,ECE PI
            ERTURK
            PC C12N15/86
            CC COOP-TF SITE
            FH Key
            Location/Qualifiers

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FT      source      1..11
      /organisms="Adenovirus"
FEATURES
      FT      Location/Qualifiers
      source      1..11
                  /organism="unidentified adenovirus"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:10535"
BASE COUNT      2 a      3 c      3 g      3 t

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 GGCCAAAGTC 20
      |||
      11 GGTCAAAGTC 2

Db

RESULT 99
A94680/c      9 bp      DNA      linear      PAT 26-JAN-2000
LOCUS
DEFINITION
Sequence 2 from Patent EP0939122.
ACCESSION
A94680
VERSION
A94680.1 GI:6778951
KEYWORDS
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 9)
AUTHORS
Mouse TCF-3 and TCF-4 and tumorigenesis related to WNT/Wingless
signaling
JOURNAL
Patent: EP 0939122-A 2 01-SEP-1999;
UNIV UTRECHT (NL)
FEATURES
      Location/Qualifiers
      source      1..9
                  /organism="unidentified"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32644"
BASE COUNT      0 a      4 c      2 g      3 t

Query Match      40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GGCCAAAG 18
      |||
      9 GGCCAAAG 2

Db

RESULT 100
AX023498      9 bp      DNA      linear      PAT 15-SEP-2000
LOCUS
DEFINITION
Sequence 2 from Patent WO0018913.
ACCESSION
AX023498
VERSION
AX023498.1 GI:10183893
KEYWORDS
SOURCE
synthetic construct
ORGANISM
synthetic construct
REFERENCE
1 (bases 1 to 9)
AUTHORS
van Es,J.H., Clevers,J.C. and Pelfer,M.A.
JOURNAL
Patent: WO 0018913-A 2 06-APR-2000;
ES JOHANNES HENDRIKUS VAN (NL); UNIV UTRECHT (NL); CLEVERS
JOHANNES CAROLUS (NL); PELFER MARK ALAN (US)
FEATURES
      Location/Qualifiers
      source      1..9
                  /organism="synthetic construct"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32630"
                  /note="mutation Fcf-responsive element"
BASE COUNT      0 a      4 c      2 g      3 t

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Query Match      40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GGCCAAAG 18
      |||
      9 GGCCAAAG 2

Db

RESULT 101
AX668925/c      9 bp      DNA      linear      PAT 26-MAR-2003
LOCUS
DEFINITION
Sequence 2374 from Patent WO0242459.
ACCESSION
AX668925
VERSION
AX668925.1 GI:29291902
KEYWORDS
SOURCE
synthetic construct
ORGANISM
synthetic construct
REFERENCE
1
AUTHORS
Liu,Q.
JOURNAL
Position dependent recognition of gmn nucleotide triplets by zinc
fingers
Patent: WO 0242459-A 2374 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
      Location/Qualifiers
      source      1..9
                  /organism="synthetic construct"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32630"
                  /note="example target DNA"
BASE COUNT      0 a      3 c      4 g      2 t

Query Match      40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CCAGGCCA 15
      |||
      9 CCAGGCCA 2

Db

RESULT 102
AX668927/c      9 bp      DNA      linear      PAT 26-MAR-2003
LOCUS
DEFINITION
Sequence 2376 from Patent WO0242459.
ACCESSION
AX668927
VERSION
AX668927.1 GI:29291904
KEYWORDS
SOURCE
synthetic construct
ORGANISM
synthetic construct
REFERENCE
1
AUTHORS
Liu,Q.
JOURNAL
Position dependent recognition of gmn nucleotide triplets by zinc
fingers
Patent: WO 0242459-A 2376 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
      Location/Qualifiers
      source      1..9
                  /organism="synthetic construct"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32630"
                  /note="example target DNA"
BASE COUNT      0 a      3 c      4 g      2 t

Query Match      40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CCAGGCCA 15
      |||

```

Db 9 CCAGGCCA 2

RESULT 103
LOCUS AX668975/c
DEFINITION Sequence 2424 from Patent WO0242459.
ACCESSION AX668975
VERSION AX668975.1 GI:29291952
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnm nucleotide triplets by zinc fingers
JOURNAL Patent: WO 0242459-A 2424 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES Location/Qualifiers
source 1..9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="example target DNA"

BASE COUNT 0 a 3 c 4 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 8 CCAGGCCA 15
Db 9 CCAGGCCA 2

RESULT 104
LOCUS AX153313
DEFINITION Sequence 1228 from Patent WO0138577.
ACCESSION AX153313
VERSION AX153313.1 GI:14534964
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1228 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 1 a 3 c 4 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GGCCAGGC 13
Db 3 GGCCAGGC 10

RESULT 105
LOCUS AX153314
DEFINITION Sequence 1229 from Patent WO0138577.
ACCESSION AX153314

VERSION AX153314.1 GI:14534965
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1229 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 1 a 3 c 4 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GGCCAGGC 13
Db 3 GGCCAGGC 10

RESULT 106
LOCUS AX153315
DEFINITION Sequence 1230 from Patent WO0138577.
ACCESSION AX153315
VERSION AX153315.1 GI:14534966
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1230 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 1 a 3 c 4 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GGCCAGGC 13
Db 3 GGCCAGGC 10

RESULT 107
LOCUS AX153316
DEFINITION Sequence 1231 from Patent WO0138577.
ACCESSION AX153316
VERSION AX153316.1 GI:14534967
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes

JOURNAL Patent: WO 0138577-A 1231 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 3 c 4 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGGC 13
|||||
3 GGCCAGGC 10

RESULT 108
AX153317 10 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 1232 from Patent WO0138577.
AX153317
VERSION AX153317.1 GI:14534968
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1232 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 3 c 4 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGGC 13
|||||
3 GGCCAGGC 10

RESULT 109
AX153318 10 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 1233 from Patent WO0138577.
AX153318
VERSION AX153318.1 GI:14534969
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1233 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 3 c 4 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGGC 13
|||||
3 GGCCAGGC 10

RESULT 110
AX153319 10 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 1234 from Patent WO0138577.
AX153319
VERSION AX153319.1 GI:14534970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1234 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGGC 13
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3 GGCCAGGC 10

RESULT 111
BD083124 10 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Human matured/activated dendritic cell expression genes.
BD083124
VERSION BD083124.1 GI:22628734
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 45 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001327293-A/45
PD 27-NOV-2001
PI KOTI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
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BASE COUNT 1 a 3 c 4 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCAGGC 13
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 Db 3 GGGCAGGC 10

RESULT 112
 BD161262 10 bp DNA linear PAT 17-JAN-2003
 LOCUS Human activated Th1 and Th2 cell expression genes.
 DEFINITION
 ACCESSION BD161262.1 GI:27867020
 VERSION
 KEYWORDS JP 2002186482-A/84
 SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE
 AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
 TITLE Human activated Th1 and Th2 cell expression genes
 JOURNAL Patent: JP 2002186482-A 84 02-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT OS Homo sapiens (human)
 PN JP 2002186482-A/84
 PD 02-JUL-2002
 PF 19-DEC-2000 JP 2000385816
 PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
 C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
 activated Th1 and Th2 cell expression genes FH Key
 Location/Qualifiers

FEATURES
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 1..10 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 3 c 4 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
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 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCAGGC 13
 |||||
 Db 3 GGGCAGGC 10

RESULT 113
 BD167212 10 bp DNA linear PAT 17-JAN-2003
 LOCUS Human liver disease-expressing genes.
 DEFINITION
 ACCESSION BD167212
 VERSION BD167212.1 GI:27873024
 KEYWORDS JP 2002209591-A/757.
 SOURCE unidentified
 ORGANISM unidentified

REFERENCE
 AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 757 30-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT OS Homo sapiens (human)
 PN JP 2002209591-A/757
 PD 30-JUL-2002
 PF 19-JAN-2001 JP 2001012328
 PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUTICHI KANEKO,TARO PI
 YAMASHITA
 PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,

PC C12P21/08,
 PC C12N15/00
 CC Human liver disease-expressing genes
 FH Key Location/Qualifiers
 FT source 1..10
 /organism="Homo sapiens (human)"

FEATURES
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 1..10 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

BASE COUNT 1 a 3 c 4 g 2 t

QY 6 GGGCAGGC 13
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 Db 3 GGGCAGGC 10

RESULT 114
 E39489 10 bp DNA linear PAT 31-JAN-2002
 LOCUS Genes with human dendritic cell expression.
 DEFINITION
 ACCESSION E39489.1 GI:18621580
 VERSION
 KEYWORDS JP 2000279181-A/22.
 SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE
 AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
 TITLE Genes with human dendritic cell expression
 JOURNAL Patent: JP 2000279181-A 22 10-OCT-2000;
 SCIENCE & TECH AGENCY
 COMMENT OS Homo sapiens (human)
 PN JP 2000279181-A/22
 PD 10-OCT-2000
 PF 01-APR-1999 JP 1999095481
 PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
 C12N15/09,C07K14/475,C07K16/18,C12N15/00

FEATURES
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 1..10 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 3 c 4 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCAGGC 13
 |||||
 Db 3 GGGCAGGC 10

RESULT 115
 E54829 10 bp DNA linear PAT 27-AUG-2002
 LOCUS Human normal liver cell expression genes.
 DEFINITION
 ACCESSION E54829
 VERSION E54829.1 GI:22556312
 KEYWORDS JP 2001211883-A/181.
 SOURCE Homo sapiens (human)

COMMENT OS Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushina,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 181 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/181
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K16/18, C12P21/02, C12N15/00
CC
FH Key Location/Qualifiers.
FEATURES
source 1..10 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 3 c 4 g 2 t
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GCCCAGC 13
Db 3 GCCCAGC 10
RESULT 116
AR058606/c 10 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 183 from patent US 5837832.
DEFINITION AR058606
ACCESSION AR058606
VERSION AR058606.1 GI:5984183
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
Lipshutz,R.U., Lohman,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 183 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
BASE COUNT 1 a 4 c 5 g 0 t
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TCCGGGCC 9
Db 8 TCCGGGCC 1
RESULT 117
AR088590/c 10 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 6 from patent US 5989906.
DEFINITION AR088590
ACCESSION AR088590
VERSION AR088590.1 GI:10015354
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TCCGGGCC 9
Db 8 TCCGGGCC 1

AUTHORS Thompson,J.D.
TITLE Method and reagent for inhibiting P-glycoprotein (mdr-1-gene)
JOURNAL Patent: US 5989906-A 6 23-NOV-1999;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
BASE COUNT 2 a 2 c 3 g 3 t
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 GCCCAACT 19
Db 10 GCCCAACT 3
RESULT 118
AX152706 10 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 621 from Patent WO0138577.
DEFINITION AX152706
ACCESSION AX152706
VERSION AX152706.1 GI:14534357
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 621 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
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/db_xref="taxon:9606"
BASE COUNT 1 a 2 c 7 g 0 t
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCCAGC 12
Db 1 GGGCCAGC 8
RESULT 119
AX152961 10 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 876 from Patent WO0138577.
DEFINITION AX152961
ACCESSION AX152961
VERSION AX152961.1 GI:14534612
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 876 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 4 c 4 g 1 t
Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GCCAGGCC 14
Db 10 GCCAGGCC 3

RESULT 120
AX152962/c
LOCUS AX152962 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 877 from Patent WO0138577.
ACCESSION AX152962
VERSION AX152962.1 GI:14534613
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 877 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
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/db_xref="taxon:9606"

BASE COUNT 1 a 4 c 4 g 1 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GCCAGGCC 14
Db 10 GCCAGGCC 3

RESULT 121
AX153299/c
LOCUS AX153299 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1214 from Patent WO0138577.
ACCESSION AX153299
VERSION AX153299.1 GI:14534950
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1214 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
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BASE COUNT 1 a 4 c 3 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GCCAGGCC 13
Db 8 GCCAGGCC 1

RESULT 122

AX153300/c
LOCUS AX153300 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1215 from Patent WO0138577.
ACCESSION AX153300
VERSION AX153300.1 GI:14534951
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1215 31-MAY-2001;
The Johns Hopkins University (US)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 1 a 4 c 3 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GCCAGGCC 13
Db 8 GCCAGGCC 1

RESULT 123
BD007922
LOCUS BD007922 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007922
VERSION BD007922.1 GI:18636295
KEYWORDS JP 2001069993-A/198.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 198 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/198
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00

FEATURES
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FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 1 a 2 c 7 g 0 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCCAGGCC 12
Db 5 GCCAGGCC 12

Db 1 GGGCCAGC 8

RESULT 124
LOCUS BD007953/c 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocytic expressing genes.
ACCESSION BD007953
VERSION BD007953.1 GI:18636326
KEYWORDS JP 2001069993-A/229.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocytic expressing genes
JOURNAL Patent: JP 2001069993-A 229 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT
OS Homo sapiens (human)
PN JP 2001069993-A/229
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00

FEATURES
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FT Location/Qualifiers
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/db_xref='taxon:9606'

BASE COUNT 1 a 4 c 3 g 2 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCCAGC 13
DB 8 GGGCCAGC 1

RESULT 125
LOCUS BD083213 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083213
VERSION BD083213.1 GI:22628823
KEYWORDS JP 2001327293-A/134.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
Human matured/activated dendritic cell expression genes
Patent: JP 2001327293-A 134 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT
OS Homo sapiens (human)
PN JP 2001327293-A/134
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
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FH Key Location/Qualifiers.

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source Location/Qualifiers
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/db_xref='taxon:9606'

BASE COUNT 3 a 3 c 4 g 0 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CAGGCCCA 16
DB 2 CAGGCCCA 9

RESULT 126
LOCUS BD083308/c 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083308
VERSION BD083308.1 GI:22628918
KEYWORDS JP 2001327293-A/229.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
Human matured/activated dendritic cell expression genes
Patent: JP 2001327293-A 229 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT
OS Homo sapiens (human)
PN JP 2001327293-A/229
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers.

FEATURES
source Location/Qualifiers
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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

BASE COUNT 1 a 4 c 4 g 1 t

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGGCCAG 11
DB 8 CCGGCCAG 1

RESULT 127
LOCUS BD161348 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161348
VERSION BD161348.1 GI:27867106
KEYWORDS JP 2002186482-A/170.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 10)
Nagai,S., Matsushima,K. and Hashimoto,S.
Human activated Th1 and Th2 cell expression genes
Patent: JP 2002186482-A 170 02-JUN-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP

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COMMENT      OS      Homo sapiens (human)
              PN      JP 2002186482-A/170
              PD      02-JUL-2002
              PF      19-DEC-2000 JP 2000385816
              PI      SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
              CI2N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC      Human
              activated tni and Th2 cell expression genes FH      Key
              Location/Qualifiers
              FT      source
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                  /organism='Homo sapiens (human)'.
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                  1..10
                  /organism='Homo sapiens'
                  /mol_type='genomic DNA'
                  /db_xref='taxon:9606'

BASE COUNT      4 a      2 c      4 g      0 t

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GGCCCAAG 18
Db      1 GGCCCAAG 8

RESULT 128
BD166572      10 bp      DNA      linear      PAT 17-JAN-2003
LOCUS      BD166572
DEFINITION      Human liver disease-expressing genes.
ACCESSION      BD166572.1 GI:27872384
VERSION      JP 2002209591-A/117.
KEYWORDS      unidentified
SOURCE      unidentified
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL      Patent: JP 2002209591-A 117 30-JUL-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS      Homo sapiens (human)
              PN      JP 2002209591-A/117
              PD      30-JUL-2002
              PF      19-JAN-2001 JP 2001012328
              PI      KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
              YAMASHITA
              PC      C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02.
              PC      C12P21/08,
              PC      C12N15/00
              CC      Human liver disease-expressing genes
              FH      Key
              FT      source
                  1..10
                  Location/Qualifiers
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                  /mol_type='genomic DNA'
                  /db_xref='taxon:32644'

BASE COUNT      5 a      2 c      3 g      0 t

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 AGGCCAAA 17
Db      2 AGGCCAAA 9

RESULT 129
BD167054      10 bp      DNA      linear      PAT 17-JAN-2003
LOCUS      BD167054

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DEFINITION      Human liver disease-expressing genes.
ACCESSION      BD167054
VERSION      BD167054.1 GI:27872866
KEYWORDS      JP 2002209591-A/599.
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL      Patent: JP 2002209591-A 599 30-JUL-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS      Homo sapiens (human)
              PN      JP 2002209591-A/599
              PD      30-JUL-2002
              PF      19-JAN-2001 JP 2001012328
              PI      KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
              YAMASHITA
              PC      C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02.
              PC      C12P21/08,
              PC      C12N15/00
              CC      Human liver disease-expressing genes
              FH      Key
              FT      source
                  1..10
                  Location/Qualifiers
                  /organism='Homo sapiens (human)'.
                  1..10
                  /organism='unidentified'
                  /mol_type='genomic DNA'
                  /db_xref='taxon:32644'

BASE COUNT      1 a      2 c      6 g      1 t

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GGCCCAAG 12
Db      3 GGCCCAAG 10

RESULT 130
E54715      10 bp      DNA      linear      PAT 27-AUG-2002
LOCUS      E54715
DEFINITION      Human normal liver cell expression genes.
ACCESSION      E54715
VERSION      E54715.1 GI:22556198
KEYWORDS      JP 2001211883-A/67.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human normal liver cell expression genes
JOURNAL      Patent: JP 2001211883-A 67 07-AUG-2001;
              SCIENCE & TECH AGENCY
COMMENT      OS      Homo sapiens (human)
              PN      JP 2001211883-A/67
              PD      07-AUG-2001
              PF      31-JAN-2000 JP 2000023170
              PI      KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
              YAMASHITA
              PC      C12N15/09,C07K16/18,C12P21/02,C12N15/00
              CC      Key
              FT      source
                  1..10
                  Location/Qualifiers
                  /organism='Homo sapiens'
                  /mol_type='genomic DNA'
                  /db_xref='taxon:9606'

BASE COUNT      3 a      3 c      4 g      0 t

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Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 CAGGCCCA 16
 2 CAGGCCCA 9

Db

RESULT 131
 AX482038
 LOCUS AX482038 11 bp DNA linear PAT 16-AUG-2002
 DEFINITION Sequence 15 from Patent EP1225233.
 ACCESSION AX482038
 VERSION AX482038.1 GI:22316760
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE 1
 AUTHORS van der Kuyt, A.C. and Cornelissen, M.
 TITLE Means and methods for treatment evaluation
 JOURNAL Patent: EP 1225233-A 15 24-JUL-2002;
 Amsterdam Support Diagnostics B.V. (NL)
 FEATURES
 source Location/Qualifiers
 1..11
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="TAG sequence Hs74649 and Hs288761"

BASE COUNT 1 a 5 c 4 g 1 t

Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 79;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCGGCCAGGCC 14
 1 CAGGCTTGCC 11

Db

RESULT 132
 AX511277
 LOCUS AX511277 11 bp DNA linear PAT 28-SEP-2002
 DEFINITION Sequence 15 from Patent WO02059558.
 ACCESSION AX511277
 VERSION AX511277.1 GI:23392154
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1
 AUTHORS van der Kuyt, A.C. and Cornelissen, M.
 TITLE Means and methods for treatment evaluation
 JOURNAL Patent: WO 02059558-A 15 01-AUG-2002;
 Amsterdam Support Diagnostics B.V. (NL)
 FEATURES
 source Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="TAG sequence Hs74649 and Hs288761"

BASE COUNT 1 a 5 c 4 g 1 t

Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 79;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCGGCCAGGCC 14
 1 CAGGCTTGCC 11

Db

RESULT 133
 AX625382
 LOCUS AX625382 11 bp DNA linear PAT 21-FEB-2003
 DEFINITION Sequence 2423 from Patent WO02053774.
 ACCESSION AX625382
 VERSION AX625382.1 GI:28453323
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE 1
 AUTHORS Petersohn, D., Conradt, M. and Hofmann, K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 2423 11-JUL-2002;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 FEATURES
 source Location/Qualifiers
 1..11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 1 a 5 c 4 g 1 t

Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 79;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCGGCCAGGCC 14
 1 CAGGCTTGCC 11

Db

RESULT 134
 AX470751
 LOCUS AX470751 11 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 328 from Patent WO02053772.
 ACCESSION AX470751
 VERSION AX470751.1 GI:22205876
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE 1
 AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
 TITLE Method for determining skin stress or skin ageing in vitro
 JOURNAL Patent: WO 02053773-A 328 11-JUL-2002;
 HENKEL KGAA (DE)
 FEATURES
 source Location/Qualifiers
 1..11
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 0 a 4 c 5 g 2 t

Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 79;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 CCGGCCAGGCC 13
 1 CTGGGCTTGGC 11

Db

RESULT 135
 AX629883
 LOCUS AX629883 11 bp DNA linear PAT 21-FEB-2003
 DEFINITION Sequence 6924 from Patent WO02053774.
 ACCESSION AX629883
 VERSION AX629883.1 GI:28457921
 KEYWORDS
 SOURCE
 ORGANISM

```

REFERENCE
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE         Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL      1
FEATURES
source       1
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             | Petersohn,D., Conradt,M. and Hofmann,K.
             | Method for determining homeostasis of the skin
             | Patent: WO 02053774-A 6924 11-JUL-2002;
             | Henkel Kommanditgesellschaft auf Aktien (DE)
             | Location/Qualifiers
             | 1..11
             | /organism="Homo sapiens"
             | /mol_type="genomic DNA"
             | /db_xref="taxon:9606"
BASE COUNT   0 a 4 c 5 g 2 t
Query Match  39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 79;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
Db           3 CCGGGCCGAGC 13
             |
             | 1 CTGGGCTGCGC 11

RESULT 136
LOCUS       ARI145684 17 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6218109.
ACCESSION  ARI145684
VERSION    ARI145684.1 GI:15108873
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Elledge,S.J. and Sanchez,Y.
TITLE     Mammalian checkpoint genes and proteins
JOURNAL   Patent: US 6218109-A 6 17-APR-2001;
FEATURES
source     1..17
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             | /organism="unknown"
BASE COUNT 5 a 4 c 5 g 3 t
Query Match 39.0%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 1,1e+02;
Matches     9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
Db           6 GGGCAGGCCAA 16
             |
             | 11 GGCCTGTCCAA 1

RESULT 137
LOCUS       ARI174508 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6307015.
ACCESSION  ARI174508
VERSION    ARI174508.1 GI:17914828
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Elledge,S.J. and Sanchez,Y.
TITLE     Mammalian checkpoint genes and proteins
JOURNAL   Patent: US 6307015-A 6 23-OCT-2001;
FEATURES
source     1..17
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             | /organism="unknown"
BASE COUNT 5 a 4 c 5 g 3 t
Query Match 39.0%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 1,1e+02;
Matches     9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY
Db           6 GGGCAGGCCAA 16
             |
             | 11 GGCCTGTCCAA 1

RESULT 138
LOCUS       ARI10470 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6114517.
ACCESSION  ARI10470
VERSION    ARI10470.1 GI:12826746
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Monta,B.P. and Xu,X.S.
TITLE     Methods of modulating tumor necrosis factor .alpha.-induced
JOURNAL   expression of cell adhesion molecules
FEATURES
source     1..20
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             | /organism="unknown"
BASE COUNT 4 a 7 c 7 g 2 t
Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 1,2e+02;
Matches    10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
Db           1 GTCGGGCCAGGCC 14
             |
             | 14 GGCCTGGCCCGGAC 1

RESULT 139
LOCUS       ARI16450 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 31 from patent US 6133246.
ACCESSION  ARI16450
VERSION    ARI16450.1 GI:14096772
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   McKay,R., Dean,N., Monta,B.P., Nero,P.S. and Gaarde,W.A.
TITLE     Antisense oligonucleotide compositions and methods for the
JOURNAL   modulation of JNK proteins
FEATURES
source     1..20
             |
             | /organism="unknown"
BASE COUNT 4 a 7 c 7 g 2 t
Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 1,2e+02;
Matches    10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
Db           1 GTCGGGCCAGGCC 14
             |
             | 14 GGCCTGGCCCGGAC 1

RESULT 140
LOCUS       ARI16461 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 42 from patent US 6133246.
ACCESSION  ARI16461
VERSION    ARI16461.1 GI:14096783
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.

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QY 1 GTCCGGGCCAGGCC 14
 Db 14 GGCCTGGCCCGGAC 1

RESULT 145
 BD074607/c 20 bp DNA linear PAT 27-AUG-2002
 LOCUS Antisense oligonucleotide composition and modulation method of JNK protein.

ACCESSION BD074607
 VERSION BD074607.1 GI:22620210
 KEYWORDS JP 2001514905-A/31.
 SOURCE synthetic construct
 ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 20)
 AUTHORS McKay, R., Dean, N., Monia, B.P., Scott, P., Nero and Gaarde, W.A.
 TITLE Antisense oligonucleotide composition and modulation method of JNK protein

JOURNAL Patent: JP 2001514905-A 31 18-SEP-2001;
 COMMENT ISIS PHARMACEUTICALS INC
 OS Artificial Sequence
 PN JP 2001514905-A/31
 PD 18-SEP-2001
 PF 07-AUG-1998 JP 2000509875
 PR 13-AUG-1997 US 08/910629
 PI ROBERT MCKAY, NICHOLAS DEAN, BRETT P MONIA, PAMELA SCOTT PI
 NERO, WILLIAM A GAARDE
 PC C1201/68, A61K31/7088, A61K48/00, A61P35/00, C12N15/09, C12P19/34,
 CC C12N15/00
 CC antisense sequence
 FH Key
 FT source

FEATURES
 source Location/Qualifiers
 1..20 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

BASE COUNT 4 a 7 c 7 g 2 t

Query Match 38.0%; Score 7.6; DB 1; Length 20;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGGCCAGGCC 14
 Db 14 GGCCTGGCCCGGAC 1

RESULT 146
 BD074618 20 bp DNA linear PAT 27-AUG-2002
 LOCUS Antisense oligonucleotide composition and modulation method of JNK protein.

ACCESSION BD074618
 VERSION BD074618.1 GI:22620221
 KEYWORDS JP 2001514905-A/42.
 SOURCE synthetic construct
 ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 20)
 AUTHORS McKay, R., Dean, N., Monia, B.P., Scott, P., Nero and Gaarde, W.A.
 TITLE Antisense oligonucleotide composition and modulation method of JNK protein

JOURNAL Patent: JP 2001514905-A 42 18-SEP-2001;
 COMMENT ISIS PHARMACEUTICALS INC
 OS Artificial Sequence
 PN JP 2001514905-A/42
 PD 18-SEP-2001
 PF 07-AUG-1998 JP 2000509875
 PR 13-AUG-1997 US 08/910629

PI ROBERT MCKAY, NICHOLAS DEAN, BRETT P MONIA, PAMELA SCOTT PI
 NERO, WILLIAM A GAARDE
 PC C1201/68, A61K31/7088, A61K48/00, A61P35/00, C12N15/09, C12P19/34,
 CC C12N15/00
 CC control sequence (sense)
 FH Key
 FT source

FEATURES
 source Location/Qualifiers
 1..20 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

BASE COUNT 2 a 7 c 7 g 4 t

Query Match 38.0%; Score 7.6; DB 1; Length 20;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGGCCAGGCC 14
 Db 7 GGCCTGGCCCGGAC 20

RESULT 147
 AX205250 9 bp DNA linear PAT 30-AUG-2001
 LOCUS Sequence 142 from Patent WO0155369.
 DEFINITION AX205250
 ACCESSION AX205250
 VERSION AX205250.1 GI:15394509
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 9)
 AUTHORS Mauro, V.P., Edelman, G.M., Chappell, G.M., Owens, G., Pinkstaff, J.K., Krushel, L. and Zhou, W.
 TITLE Synthetic internal ribosome entry sites and methods of identifying same
 JOURNAL Patent: WO 0155369-A 142 02-AUG-2001;
 The Scripps Research Institute (US); The Neurosciences Institute (US)

FEATURES
 source Location/Qualifiers
 1..9 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="random 9 nt sequence"

BASE COUNT 1 a 3 c 4 g 1 t

Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 3e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCCGGGCC 9
 Db 1 GTCCGGGAC 9

RESULT 148
 AX668699 9 bp DNA linear PAT 26-MAR-2003
 LOCUS Sequence 2148 from Patent WO0242459.
 ACCESSION AX668699
 VERSION AX668699.1 GI:22921674
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Liu, Q.
 TITLE Position dependent recognition of gnm nucleotide triplets by zinc fingers

JOURNAL Patent: WO 0242459-A 2148 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES Location/Qualifiers
source 1..9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="example target DNA"

BASE COUNT 1 a 2 c 6 g 0 t

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGC 13
|||||
1 GGGCCAGC 9

Db 1 GGGCCAGC 9

RESULT 149
AX668700 9 bp DNA linear PAT 26-MAR-2003
LOCUS
DEFINITION Sequence 2149 from Patent WO0242459.
ACCESSION AX668700
VERSION AX668700.1 GI:29291675
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Liu Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
JOURNAL fingers
Patent: WO 0242459-A 2149 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES Location/Qualifiers
source 1..9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="example target DNA"

BASE COUNT 1 a 2 c 6 g 0 t

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGC 13
|||||
1 GGGCCAGC 9

Db 1 GGGCCAGC 9

RESULT 150
AX224404 10 bp DNA linear PAT 10-SEP-2001
LOCUS
DEFINITION Sequence 11 from Patent WO0160997.
ACCESSION AX224404
VERSION AX224404.1 GI:15554646
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 11 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Zea mays"
/mol_type="genomic DNA"

BASE COUNT 0 a 5 c 5 g 0 t

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGCCAG 11
|||||
2 CCGGCCCG 10

Db 2 CCGGCCCG 10

RESULT 151
AX224407 10 bp DNA linear PAT 10-SEP-2001
LOCUS
DEFINITION Sequence 14 from Patent WO0160997.
ACCESSION AX224407
VERSION AX224407.1 GI:15554649
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 14 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"

BASE COUNT 0 a 5 c 5 g 0 t

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGCCAG 11
|||||
9 CCGGCCCG 1

Db 9 CCGGCCCG 1

RESULT 152
AX224410 10 bp DNA linear PAT 10-SEP-2001
LOCUS
DEFINITION Sequence 17 from Patent WO0160997.
ACCESSION AX224410
VERSION AX224410.1 GI:15554652
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 17 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"

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Qy      1 GTCCGGGCC 9
Db      1 GCGCGGGCC 9

RESULT 153
LOCUS   AX153299
DEFINITION Sequence 1214 from Patent WO01385577.
ACCESSION AX153299
VERSION   AX153299.1 GI:14534950
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS  Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLES   Human transcriptomes
JOURNAL  Patent: WO 0138577-A 1214 31-MAY-2001;
          The Johns Hopkins University (US)
FEATURES
  source
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

BASE COUNT      1 a      4 c      3 g      2 t

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GCCAGGCCA 15
Db      1 GCCTGGCCA 9

RESULT 154
LOCUS   AX153300
DEFINITION Sequence 1215 from Patent WO01385577.
ACCESSION AX153300
VERSION   AX153300.1 GI:14534951
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS  Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLES   Human transcriptomes
JOURNAL  Patent: WO 0138577-A 1215 31-MAY-2001;
          The Johns Hopkins University (US)
FEATURES
  source
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

BASE COUNT      1 a      4 c      3 g      2 t

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GCCAGGCCA 15
Db      1 GCCTGGCCA 9

RESULT 155
LOCUS   BD007953
DEFINITION lps activated human monocyte expressing genes.

```

```

ACCESSION BD007953
VERSION   BD007953.1 GI:18636326
KEYWORDS  JP 200106993-A/229.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens (human)

REFERENCE
AUTHORS  Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLES   lps activated human monocyte expressing genes
JOURNAL  Patent: JP 200106993-A 229 21-MAR-2001;
          JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT
OS Homo sapiens (human)
PN JP 200106993-A/229
PD 21-MAR-2001
PE 28-APR-2000 JP 2000331079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key
FT source
FT Location/Qualifiers

FEATURES
  source
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

BASE COUNT      1 a      4 c      3 g      2 t

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GCCAGGCCA 15
Db      1 GCCTGGCCA 9

RESULT 156
LOCUS   AX625842/c
DEFINITION Sequence 2883 from Patent WO2053774.
ACCESSION AX625842
VERSION   AX625842.1 GI:28453878
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLES   Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 2883 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    1..11
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

BASE COUNT      1 a      4 c      4 g      2 t

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GCCAGGCCA 15
Db      10 GCCTGGCCA 2

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RESULT 157
AX630156 11 bp DNA linear PAT 21-FEB-2003
LOCUS
DEFINITION Sequence 7197 from Patent WO02053774.
ACCESSION AX630156
VERSION AX630156.1 GI:28458194
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7197 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 0 a 3 c 5 g 3 t

Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGC 13
|||||
2 GGGCCTGGC 10

Db

RESULT 158
AX129247 19 bp DNA linear PAT 15-MAY-2001
LOCUS
DEFINITION Sequence 465 from Patent WO0130362.
ACCESSION AX129247
VERSION AX129247.1 GI:14135552
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 465 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source 1. .19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="Cdk4 ribozyme binding site"

BASE COUNT 1 a 6 c 7 g 5 t

Query Match 37.0%; Score 7.4; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGGCAGGCC 14
|||||
11 GGCCCTGGC 19

Db

RESULT 159
AX017438/c 9 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 13 from Patent WO9947656.
ACCESSION AX017438
VERSION AX017438.1 GI:10042250
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 9)
AUTHORS Isalan,M. and Choo,Y.
JOURNAL Nucleic acid binding proteins
Patent: WO 9947656-A 13 23-SEP-1999;
MEDICAL RES COUNCIL (GB); ISALAN MARK (GB); CHOO YEN (GB)
FEATURES
source 1. .9
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT 0 a 4 c 5 g 0 t

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGGGCC 9
|||||
Db 7 CCGGGCC 1

RESULT 160
AX538878/c 9 bp DNA linear PAT 23-NOV-2002
LOCUS
DEFINITION Sequence 12 from Patent WO0208436.
ACCESSION AX538878
VERSION AX538878.1 GI:25271599
KEYWORDS
SOURCE unidentified adenovirus
ORGANISM unidentified adenovirus
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

REFERENCE
AUTHORS Zhang,W.W., Alemany,R., Dai,Y., Josephs,S., Balague,C., Ayares,D.
and Schneiderman,R.
TITLE Mint-adenoviral vector system for vaccination
JOURNAL Patent: WO 0208436-A 12 31-JAN-2002;
Genstar Therapeutics Corporation (US)
FEATURES
source 1. .9
Location/Qualifiers
/organism="unidentified adenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10535"

BASE COUNT 1 a 1 c 4 g 3 t

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CAAAGTC 20
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Db 9 CAAAGTC 3

RESULT 161
AX668947/c 9 bp DNA linear PAT 26-MAR-2003
LOCUS
DEFINITION Sequence 2396 from Patent WO0242459.
ACCESSION AX668947
VERSION AX668947.1 GI:29291924
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers
JOURNAL Patent: WO 0242459-A 2396 30-MAY-2002;

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FEATURES
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    Sangamo Biosciences Inc. (US)
    Location/Qualifiers
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        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="example target DNA"
BASE COUNT
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  3 g
  3 t
  Query Match
    Best Local Similarity 100.0%; Pred. No. 3e+02;
  Matches
    7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
  12 GCCAAG 18
  8 GCCAAG 2
  Db

RESULT 162
AX668948
LOCUS
  Sequence 2397 from Patent WO0242459.
DEFINITION
  AX668948
ACCESSION
  AX668948.1 GI:29291925
KEYWORDS
  .
SOURCE
  synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
REFERENCE
  1
  AUTHORS
    Liu, Q.
  TITLE
    Position dependent recognition of gnn nucleotide triplets by zinc
    fingers
  JOURNAL
    Patent: WO 0242459-A 2397 30-MAY-2002;
  FEATURES
    source
      Location/Qualifiers
        1..9
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          /mol_type="genomic DNA"
          /db_xref="taxon:32630"
          /note="example target DNA"
BASE COUNT
  1 a
  2 c
  3 g
  3 t
  Query Match
    Best Local Similarity 100.0%; Pred. No. 3e+02;
  Matches
    7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
  12 GCCAAG 18
  8 GCCAAG 2
  Db

RESULT 163
BD138429/c
LOCUS
  Nucleic acid binding proteins.
DEFINITION
  BD138429
ACCESSION
  BD138429.1 GI:2323374
VERSION
  JP 2002506640-A/4.
KEYWORDS
  .
SOURCE
  synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
REFERENCE
  1 (bases 1 to 9)
  AUTHORS
    Choo, Y. and Isalan, M.
  TITLE
    Nucleic acid binding proteins
  JOURNAL
    Patent: JP 2002506640-A 4 05-MAR-2002;
  FEATURES
    source
      Location/Qualifiers
        1..9
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          /mol_type="genomic DNA"
          /db_xref="taxon:32630"
          /note="example target DNA"
BASE COUNT
  1 a
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  3 g
  3 t
  Query Match
    Best Local Similarity 100.0%; Pred. No. 3e+02;
  Matches
    7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
  12 GCCAAG 18
  8 GCCAAG 2
  Db

RESULT 164
AX471339/c
LOCUS
  Sequence 916 from Patent WO02053773.
DEFINITION
  AX471339
ACCESSION
  AX471339.1 GI:22206464
KEYWORDS
  .
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1
  AUTHORS
    Hofmann, K., Conradt, M. and Petersohn, P.
  TITLE
    Method for determining skin stress or skin ageing in vitro
  JOURNAL
    Patent: WO 02053773-A 916 11-JUL-2002;
  FEATURES
    source
      Location/Qualifiers
        1..11
          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"
BASE COUNT
  4 a
  4 c
  2 g
  1 t
  Query Match
    Best Local Similarity 100.0%; Pred. No. 1.2e+02;
  Matches
    7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
  6 GCCCAGG 12
  7 GCCCAGG 1
  Db

RESULT 165
AX623782/c
LOCUS
  Sequence 823 from Patent WO02053774.
DEFINITION
  AX623782
ACCESSION
  AX623782.1 GI:28451723
VERSION
  .
KEYWORDS
  .
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1
  AUTHORS
    Petersohn, P., Conradt, M. and Hofmann, K.
  TITLE
    Method for determining homeostasis of the skin
  JOURNAL
    Patent: WO 02053774-A 823 11-JUL-2002;
  FEATURES
    source
      Location/Qualifiers
        1..11
          /organism="Homo sapiens"
          /mol_type="genomic DNA"

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PC C12N15/09,C07K14/00,C12P21/02,C12N15/00
CC description of artificial sequence: Synthetic sequence FH
Key Location/Qualifiers
FT source 1..9
  /organism="Artificial Sequence".
FEATURES
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      1..9
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
BASE COUNT
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  4 c
  5 g
  0 t
  Query Match
    Best Local Similarity 100.0%; Pred. No. 3e+02;
  Matches
    7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
  3 CCGGCC 9
  7 CCGGCC 1
  Db

RESULT 164
AX471339
LOCUS
  Sequence 916 from Patent WO02053773.
DEFINITION
  AX471339
ACCESSION
  AX471339.1 GI:22206464
KEYWORDS
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SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1
  AUTHORS
    Hofmann, K., Conradt, M. and Petersohn, P.
  TITLE
    Method for determining skin stress or skin ageing in vitro
  JOURNAL
    Patent: WO 02053773-A 916 11-JUL-2002;
  FEATURES
    source
      Location/Qualifiers
        1..11
          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"
BASE COUNT
  4 a
  4 c
  2 g
  1 t
  Query Match
    Best Local Similarity 100.0%; Pred. No. 1.2e+02;
  Matches
    7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
  6 GCCCAGG 12
  7 GCCCAGG 1
  Db

RESULT 165
AX623782
LOCUS
  Sequence 823 from Patent WO02053774.
DEFINITION
  AX623782
ACCESSION
  AX623782.1 GI:28451723
VERSION
  .
KEYWORDS
  .
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1
  AUTHORS
    Petersohn, P., Conradt, M. and Hofmann, K.
  TITLE
    Method for determining homeostasis of the skin
  JOURNAL
    Patent: WO 02053774-A 823 11-JUL-2002;
  FEATURES
    source
      Location/Qualifiers
        1..11
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          /mol_type="genomic DNA"

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BASE COUNT      4 a      4 c      2 g      1 t
/db_xref="taxon:9606"

Query Match      35.0%; Score 7; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGCAGG 12
        |||||
        7 GGGCAGG 1

Db

RESULT 166
AX631203/c      11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION      Sequence 8245 from Patent WO02053774.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 8245 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    1..11
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    /mol_type="genomic DNA"
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BASE COUNT      4 a      4 c      2 g      1 t

Query Match      35.0%; Score 7; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGCAGG 12
        |||||
        7 GGGCAGG 1

Db

RESULT 167
AX152961      10 bp      DNA      linear      PAT 22-JUN-2001
LOCUS
DEFINITION      Sequence 876 from Patent WO0138577.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  Human transcripts
  Patent: WO 0138577-A 876 31-MAY-2001;
  The Johns Hopkins University (US)
FEATURES
  source
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

BASE COUNT      1 a      4 c      4 g      1 t

Query Match      34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CGGGCCAGG 13
        |||||
        4 CGGGCCAGG 13

Db

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Db      1 CAGGCTGGC 10

RESULT 168
AX152962      10 bp      DNA      linear      PAT 22-JUN-2001
LOCUS
DEFINITION      Sequence 877 from Patent WO0138577.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  Human transcripts
  Patent: WO 0138577-A 877 31-MAY-2001;
  The Johns Hopkins University (US)
FEATURES
  source
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    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

BASE COUNT      1 a      4 c      4 g      1 t

Query Match      34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CGGGCCAGG 13
        |||||
        1 CAGGCTGGC 10

Db

RESULT 169
AX629507      11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION      Sequence 6548 from Patent WO02053774.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 6548 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    1..11
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

BASE COUNT      1 a      5 c      3 g      2 t

Query Match      34.0%; Score 6.8; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGGCAGGCCA 15
        |||||
        2 GGCTGCGCCA 11

Db

RESULT 170
E63474      8 bp      DNA      linear      PAT 27-AUG-2002
LOCUS
DEFINITION      Non-human animal having modified foreign chromosomal or slice
  thereof.
ACCESSION
E63474

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VERSION E63474.1 GI:22557583
KEYWORDS JP 2001231403-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 8)
AUTHORS Tomizuka, K., Yoshida, H., Ishida, I. and Kuroiwa, Y.
TITLE Non-human animal having modified foreign chromosomal or slice
JOURNAL Patent: JP 2001231403-A 6 28-AUG-2001;
KIRIN BEER KK
COMMENT OS Artificial Sequence
PN JP 2001231403-A/6
PD 28-AUG-2001
PF 18-FEB-2000 JP 2000042074
PI KAZUMA TOMIZUKA, HITOSHI YOSHIDA, ISAO ISHIDA, YOSHIMI KUROIWA PC
A01K67/027, C12N5/10, C12N15/09// (C12N5/10, C12R1:91), (C12N15/09, C12R1:91)
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91), (C12N15/00, C12R1:91) CC
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Location/Qualifiers
1..8
location/Qualifiers
source
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Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCCGGGC 8
| | | | |
1 GCCCGGCG 8
Db
RESULT 171
E63474/c
LOCUS E63474
DEFINITION Non-human animal having modified foreign chromosomal or slice
thereof.
ACCESSION E63474
VERSION E63474.1 GI:22557583
KEYWORDS JP 2001231403-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 8)
AUTHORS Tomizuka, K., Yoshida, H., Ishida, I. and Kuroiwa, Y.
TITLE Non-human animal having modified foreign chromosomal or slice
JOURNAL Patent: JP 2001231403-A 6 28-AUG-2001;
KIRIN BEER KK
COMMENT OS Artificial Sequence
PN JP 2001231403-A/6
PD 28-AUG-2001
PF 18-FEB-2000 JP 2000042074
PI KAZUMA TOMIZUKA, HITOSHI YOSHIDA, ISAO ISHIDA, YOSHIMI KUROIWA PC
A01K67/027, C12N5/10, C12N15/09// (C12N5/10, C12R1:91), (C12N15/09, C12R1:91)
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91), (C12N15/00, C12R1:91) CC
Description of Artificial Sequence: SfiI linker FH Key
Location/Qualifiers
1..8
location/Qualifiers
source
FEATURES
BASE COUNT 0 a 4 c 4 g 0 t
Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCCGGGC 8
| | | | |
8 GCCCGGCG 1
Db

Search completed: November 10, 2003, 07:57:04
Job time: 1 secs

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2003, 08:01:31 ; Search time 1 Seconds
(without alignments)
0.102 Million cell updates/sec

Title: us-09-774-809-31

Perfect score: 20

Sequence: 1 gtcgsgccagcagcaagtc 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 232 seqs, 2559 residues

Total number of hits satisfying chosen parameters: 464

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : rng.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20 1	AAZ29331
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5	20	100.0	20 1	AAZ29331
6	20	100.0	20 1	AAZ29331
7	20	100.0	20 1	AAZ29331
8	20	100.0	20 1	AAZ29331
9	20	100.0	20 1	AAZ29331
10	20	100.0	20 1	AAZ29331
11	20	100.0	20 1	AAZ29331
12	20	100.0	20 1	AAZ29331
13	20	100.0	20 1	AAZ29331
14	20	100.0	20 1	AAZ29331
15	20	100.0	20 1	AAZ29331
16	20	100.0	20 1	AAZ29331
17	20	100.0	20 1	AAZ29331
18	20	100.0	20 1	AAZ29331
19	20	100.0	20 1	AAZ29331
20	20	100.0	20 1	AAZ29331
21	20	100.0	20 1	AAZ29331
22	20	100.0	20 1	AAZ29331
23	20	100.0	20 1	AAZ29331
24	20	100.0	20 1	AAZ29331
25	20	100.0	20 1	AAZ29331
26	20	100.0	20 1	AAZ29331
27	20	100.0	20 1	AAZ29331
28	20	100.0	20 1	AAZ29331
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33	20	100.0	20 1	AAZ29331

34	10	50.0	12 1	ABZ72939	Rod opsin hamme
35	9.8	49.0	13 1	AAZ63772	Human JAGGED1 exon
36	9.8	49.0	13 1	AAZ63772	Tensin-C phospho
37	9.8	49.0	13 1	AAZ63772	Tensin-C phospho
38	9.8	49.0	13 1	AAZ63772	Oligonucleotide SE
39	9.8	49.0	13 1	AAZ63772	Oligonucleotide SE
40	9.4	47.0	11 1	AAZ63772	Murine MRL SAGE ta
41	9.4	47.0	11 1	AAZ63772	C/EBP-beta antisen
42	9.4	47.0	11 1	AAZ63772	Human C/EBP polyu
43	9.4	47.0	11 1	AAZ63772	Oligonucleotide #2
44	9.4	47.0	11 1	AAZ63772	Human adenosine re
45	9.4	47.0	11 1	AAZ63772	Human skin EST 166
46	9.4	47.0	11 1	AAZ63772	Human skin EST 442
47	9.4	47.0	11 1	AAZ63772	Human skin EST 758
48	9.4	47.0	11 1	AAZ63772	C/EBP-beta antisen
49	9.4	47.0	11 1	AAZ63772	Human C/EBP polyu
50	9.4	47.0	11 1	AAZ63772	Human adenosine re
51	9.4	47.0	11 1	AAZ63772	Human dendritic ce
52	9.4	47.0	11 1	AAZ63772	Metastatic breast
53	9.4	47.0	11 1	AAZ63772	Metastatic breast
54	9.4	47.0	11 1	AAZ63772	Metastatic breast
55	9.4	47.0	11 1	AAZ63772	Metastatic breast
56	9.4	47.0	11 1	AAZ63772	Metastatic breast
57	9.4	47.0	11 1	AAZ63772	Metastatic breast
58	9.4	47.0	11 1	AAZ63772	Metastatic breast
59	9.4	47.0	11 1	AAZ63772	Metastatic breast
60	9.4	47.0	11 1	AAZ63772	Metastatic breast
61	9.4	47.0	11 1	AAZ63772	Metastatic breast
62	9.4	47.0	11 1	AAZ63772	Metastatic breast
63	9.4	47.0	11 1	AAZ63772	Metastatic breast
64	9.4	47.0	11 1	AAZ63772	Metastatic breast
65	9.4	47.0	11 1	AAZ63772	Metastatic breast
66	9.4	47.0	11 1	AAZ63772	Metastatic breast
67	9.4	47.0	11 1	AAZ63772	Metastatic breast
68	9.4	47.0	11 1	AAZ63772	Metastatic breast
69	9.4	47.0	11 1	AAZ63772	Metastatic breast
70	9.4	47.0	11 1	AAZ63772	Metastatic breast
71	9.4	47.0	11 1	AAZ63772	Metastatic breast
72	9.4	47.0	11 1	AAZ63772	Metastatic breast
73	9.4	47.0	11 1	AAZ63772	Metastatic breast
74	9.4	47.0	11 1	AAZ63772	Metastatic breast
75	9.4	47.0	11 1	AAZ63772	Metastatic breast
76	9.4	47.0	11 1	AAZ63772	Metastatic breast
77	9.4	47.0	11 1	AAZ63772	Metastatic breast
78	9.4	47.0	11 1	AAZ63772	Metastatic breast
79	9.4	47.0	11 1	AAZ63772	Metastatic breast
80	9.4	47.0	11 1	AAZ63772	Metastatic breast
81	9.4	47.0	11 1	AAZ63772	Metastatic breast
82	9.4	47.0	11 1	AAZ63772	Metastatic breast
83	9.4	47.0	11 1	AAZ63772	Metastatic breast
84	9.4	47.0	11 1	AAZ63772	Metastatic breast
85	9.4	47.0	11 1	AAZ63772	Metastatic breast
86	9.4	47.0	11 1	AAZ63772	Metastatic breast
87	9.4	47.0	11 1	AAZ63772	Metastatic breast
88	9.4	47.0	11 1	AAZ63772	Metastatic breast
89	9.4	47.0	11 1	AAZ63772	Metastatic breast
90	9.4	47.0	11 1	AAZ63772	Metastatic breast
91	9.4	47.0	11 1	AAZ63772	Metastatic breast
92	9.4	47.0	11 1	AAZ63772	Metastatic breast
93	9.4	47.0	11 1	AAZ63772	Metastatic breast
94	9.4	47.0	11 1	AAZ63772	Metastatic breast
95	9.4	47.0	11 1	AAZ63772	Metastatic breast
96	9.4	47.0	11 1	AAZ63772	Metastatic breast
97	9.4	47.0	11 1	AAZ63772	Metastatic breast
98	9.4	47.0	11 1	AAZ63772	Metastatic breast
99	9.4	47.0	11 1	AAZ63772	Metastatic breast
100	9.4	47.0	11 1	AAZ63772	Metastatic breast
101	9.4	47.0	11 1	AAZ63772	Metastatic breast
102	9.4	47.0	11 1	AAZ63772	Metastatic breast
103	9.4	47.0	11 1	AAZ63772	Metastatic breast
104	9.4	47.0	11 1	AAZ63772	Metastatic breast
105	9.4	47.0	11 1	AAZ63772	Metastatic breast
106	9.4	47.0	11 1	AAZ63772	Metastatic breast

C 107	8.4	42.0	10	1	AAH64394	Human ubiquitously
C 108	8.4	42.0	10	1	AAH32882	LPS activated huma
C 109	8.4	42.0	10	1	AAH74058	Human SLC6A4 allel
C 110	8.4	42.0	10	1	AAH33342	Yeast NORF gene SA
C 111	8.4	42.0	10	1	AAH33708	Yeast NORF gene SA
C 112	8.4	42.0	10	1	AAH34406	Yeast NORF gene SA
C 113	8.4	42.0	10	1	AAH35939	Yeast NORF gene SA
C 114	8.4	42.0	10	1	AAH41896	Yeast NORF gene SA
C 115	8.4	42.0	10	1	AAH42385	Yeast NORF gene SA
C 116	8.4	42.0	10	1	AAH43779	Yeast NORF gene SA
C 117	8.4	42.0	10	1	ABH64222	Human heat shock p
C 118	8.4	42.0	10	1	ABH64641	Human HCC/chronic
C 119	8.4	42.0	10	1	ABH64947	Human multiple HCC
C 120	8.4	42.0	10	1	ABH78373	Human Th2 cell SAG
C 121	8.4	42.0	10	1	ABH95837	Solute Carrier Fam
C 122	8.4	42.0	10	1	ABH95838	Solute Carrier Fam
C 123	8.4	42.0	10	1	ABA97040	ZP36 extension pr
C 124	8.4	42.0	10	1	ABH64054	Human BF gene alle
C 125	8.4	42.0	10	1	AAH19876	Oligonucleotide #5
C 126	8.4	42.0	10	1	ABH23567	Transcript tag DNA
C 127	8.4	42.0	10	1	ABH24232	Retinaldehyde-bind
C 128	8.4	42.0	10	1	AAH99275	Human F12 gene all
C 129	8.4	42.0	10	1	AAH16750	Human APOA4 A50, p
C 130	8.4	42.0	10	1	ABH42671	Human maturation/a
C 131	8.4	42.0	11	1	ABH62380	Human skin EST 166
C 132	8.4	42.0	11	1	ABH69801	Human skin EST 758
C 133	8.4	42.0	11	1	AAH54916	C/EBP-beta antisen
C 134	8.4	42.0	11	1	AAH20485	Human C/EBP polyu
C 135	8.4	42.0	11	1	AAH43363	Human adenosine re
C 136	8.4	42.0	11	1	AAH59919	CouP-TF inverted r
C 137	8.4	42.0	11	1	ABH81854	Kaposi's Sarcoma S
C 138	8.4	42.0	11	1	ABH62551	Human skin EST 337
C 139	8.4	42.0	11	1	ABH62704	Human skin EST 490
C 140	8.4	42.0	11	1	ABH63037	Human skin EST 823
C 141	8.4	42.0	11	1	ABH65097	Human skin EST 288
C 142	8.4	42.0	11	1	ABH65146	Human skin EST 293
C 143	8.4	42.0	11	1	ABH65638	Human skin EST 342
C 144	8.4	42.0	11	1	ABH65978	Human skin EST 376
C 145	8.4	42.0	11	1	ABH66142	Human skin EST 392
C 146	8.4	42.0	11	1	ABH66964	Human skin EST 475
C 147	8.4	42.0	11	1	ABH67427	Human skin EST 521
C 148	8.4	42.0	11	1	ABH67547	Human skin EST 533
C 149	8.4	42.0	11	1	ABH68518	Human skin EST 630
C 150	8.4	42.0	11	1	ABH68762	Human skin EST 654
C 151	8.4	42.0	11	1	ABH69053	Human skin EST 683
C 152	8.4	42.0	11	1	ABH69138	Human skin EST 692
C 153	8.4	42.0	11	1	ABH69411	Human skin EST 719
C 154	8.4	42.0	11	1	ABH69528	Human skin EST 731
C 155	8.4	42.0	11	1	ABH69972	Human skin EST 775
C 156	8.4	42.0	11	1	ABH70125	Human skin EST 791
C 157	8.4	42.0	11	1	ABH70458	Human skin EST 824
C 158	8.4	42.0	11	1	ABH68459	Human skin stress/
C 159	8.4	42.0	11	1	ABH68573	Human skin stress/
C 160	8.4	42.0	11	1	ABH687161	Human skin stress/
C 161	8.4	42.0	11	1	ABH687207	Human skin stress/
C 162	8.4	42.0	11	1	ABH692021	Short human Tumour
C 163	8.4	42.0	11	1	ABH71946	DNA tag used to id
C 164	8.4	42.0	8	1	AAH80792	A. thaliana primer
C 165	8.4	42.0	9	1	AAH63091	Human Tcf mutant D
C 166	8.4	42.0	9	1	AAH69683	Tcf optimal respon
C 167	8.4	42.0	9	1	ABH72076	Zinc finger protei
C 168	8.4	42.0	9	1	ABH72078	Zinc finger protei
C 169	8.4	42.0	9	1	ABH72126	Zinc finger protei
C 170	8.4	42.0	10	1	AAH73935	Human dendritic ce
C 171	8.4	42.0	10	1	ABA06204	Human normal hepat
C 172	8.4	42.0	10	1	AAH64388	Human ubiquitously
C 173	8.4	42.0	10	1	AAH64389	Human ubiquitously
C 174	8.4	42.0	10	1	AAH64390	Human ubiquitously
C 175	8.4	42.0	10	1	AAH64391	Human ubiquitously
C 176	8.4	42.0	10	1	AAH64392	Human ubiquitously
C 177	8.4	42.0	10	1	AAH64393	Human ubiquitously
C 178	8.4	42.0	10	1	AAH64394	Human ubiquitously
C 179	8.4	42.0	10	1	ABH64947	Human multiple HCC
C 180	8.4	42.0	10	1	ABH78373	Human Th2 cell SAG
C 181	8.4	42.0	10	1	ABH42671	Human maturation/a
C 182	8.4	42.0	10	1	AAH51821	mdr-1 mRNA ribozym
C 183	8.4	42.0	10	1	AAH66792	HIV-1 N4-3 net ge
C 184	8.4	42.0	10	1	AAH66793	HIV-1 N4-3 net ge
C 185	8.4	42.0	10	1	AAH68880	Human mitochondria
C 186	8.4	42.0	10	1	AAH54584	Human beta tryptas
C 187	8.4	42.0	10	1	AAH18625	p53 serial analysi
C 188	8.4	42.0	10	1	AAH20153	Human beta tryptas
C 189	8.4	42.0	10	1	AAH56555	Human macrophage g
C 190	8.4	42.0	10	1	AAH34031	Human adenosine re
C 191	8.4	42.0	10	1	AAH77634	Human dendritic ce
C 192	8.4	42.0	10	1	AAH279103	Human dendritic ce
C 193	8.4	42.0	10	1	AAH279322	Human dendritic ce
C 194	8.4	42.0	10	1	AAH281594	Metastatic breast
C 195	8.4	42.0	10	1	AAH282082	Metastatic breast
C 196	8.4	42.0	10	1	AAH283064	Metastatic breast
C 197	8.4	42.0	10	1	AAH283312	Metastatic breast
C 198	8.4	42.0	10	1	AAH283787	Metastatic breast
C 199	8.4	42.0	10	1	AAH283855	Metastatic breast
C 200	8.4	42.0	10	1	AAH283864	Metastatic breast
C 201	8.4	42.0	10	1	AAH284284	Metastatic breast
C 202	8.4	42.0	10	1	AAH285316	Metastatic breast
C 203	8.4	42.0	10	1	AAH285453	Metastatic breast
C 204	8.4	42.0	10	1	AAH285585	Metastatic breast
C 205	8.4	42.0	10	1	AAH285596	Metastatic breast
C 206	8.4	42.0	10	1	AAH285958	Metastatic breast
C 207	8.4	42.0	10	1	ABA06090	Human normal hepat
C 208	8.4	42.0	10	1	AAH63781	Human ubiquitously
C 209	8.4	42.0	10	1	AAH64036	Human ubiquitously
C 210	8.4	42.0	10	1	AAH64037	Human ubiquitously
C 211	8.4	42.0	10	1	AAH643374	Human ubiquitously
C 212	8.4	42.0	10	1	AAH64375	Human ubiquitously
C 213	8.4	42.0	10	1	AAH32825	LPS activated huma
C 214	8.4	42.0	10	1	AAH32856	LPS activated huma
C 215	8.4	42.0	10	1	AAH39487	Yeast NORF gene SA
C 216	8.4	42.0	10	1	AAH41493	Yeast NORF gene SA
C 217	8.4	42.0	10	1	ABH84307	Human chronic hepa
C 218	8.4	42.0	10	1	ABH84789	Human gamma-glutam
C 219	8.4	42.0	10	1	ABH78459	Human Th1 cell pre
C 220	8.4	42.0	10	1	ABH57664	Human SCY24 prime
C 221	8.4	42.0	10	1	ABH95840	Solute Carrier Fam
C 222	8.4	42.0	10	1	ABH72637	Leukotriene B4 rec
C 223	8.4	42.0	10	1	ABH17015	Pyridoxal (Pyridox
C 224	8.4	42.0	10	1	AAH599416	Aldehyde dehydroge
C 225	8.4	42.0	10	1	AAH595685	Superoxide dismuta
C 226	8.4	42.0	10	1	ABH36370	Human lysosomal ac
C 227	8.4	42.0	10	1	ABH42760	Human maturation/a
C 228	8.4	42.0	10	1	ABH42855	Human maturation/a
C 229	8.4	42.0	11	1	ABH81865	Kaposi's Sarcoma S
C 230	8.4	42.0	11	1	ABH64637	Human skin EST 242
C 231	8.4	42.0	11	1	ABH69138	Human skin EST 692
C 232	8.4	42.0	11	1	ABH68573	Human skin stress/
C 233	8.4	42.0	12	1	ABH72939	Rod opsin hammehe
C 234	8.4	42.0	17	1	AAH03853	Human cell cycle c
C 235	8.4	42.0	17	1	AAH18424	Degenerate PCR pri
C 236	8.4	42.0	17	1	ABH16354	Human checkpoint g
C 237	8.4	42.0	20	1	AAH29342	Chemically modifie
C 238	8.4	42.0	20	1	AAH29331	JNK-specific prob
C 239	8.4	42.0	20	1	AAH62874	JNK antisense Olig
C 240	8.4	42.0	20	1	AAH62885	JNK antisense Olig
C 241	8.4	42.0	20	1	AAH48651	Antisense Oligonuc
C 242	8.4	42.0	20	1	AAH23754	JNK1 antisense oli
C 243	8.4	42.0	20	1	AAH99183	Immunostimulatory
C 244	8.4	42.0	20	1	ABH77827	Angiogenesis inhib
C 245	8.4	42.0	20	1	ABH39057	Immunostimulatory
C 246	8.4	42.0	9	1	AAH54706	Human fibronectin
C 247	8.4	42.0	9	1	AAH20275	Human fibronectin
C 248	8.4	42.0	9	1	AAH34153	Human adenosine re
C 249	8.4	42.0	9	1	ABH71850	Zinc finger protei
C 250	8.4	42.0	9	1	ABH71851	Zinc finger protei
C 251	8.4	42.0	10	1	AAH28238	Metastatic breast
C 252	8.4	42.0	10	1	AAH77977	Human dendritic ce

253	7.4	37.0	10	1	AA284966	Metastatic breast
254	7.4	37.0	10	1	AAH76342	2. may5 Ms45 promo
255	7.4	37.0	10	1	AAH76345	2. may5 Ms45 promo
256	7.4	37.0	10	1	AAH76348	2. may5 Ms45 promo
257	7.4	37.0	10	1	AAH19876	Oligonucleotide #5
258	7.4	37.0	10	1	AAH64374	Human ubiquitously
259	7.4	37.0	10	1	AAH64375	Human ubiquitously
260	7.4	37.0	10	1	AAH32856	IPS activated huma
261	7.4	37.0	10	1	ABK95840	Solute Carrier Fam
262	7.4	37.0	11	1	ABV65097	Human skin EST 288
263	7.4	37.0	11	1	ABV69411	Human skin EST 719
264	7.4	37.0	19	1	AAH82879	cdk4 ribozyme bind
265	7.4	37.0	19	1	AAH58041	Cell-cytle depend
266	7.4	37.0	8	1	AAH58041	3'-primer used for
267	7.4	37.0	8	1	AAH58041	3'-primer used for
268	7.4	37.0	8	1	AAH58041	3'-primer used for
269	7.4	37.0	8	1	AAH58041	3'-primer used for
270	7.4	37.0	8	1	AAH58041	3'-primer used for
271	7.4	37.0	8	1	AAH58041	3'-primer used for
272	7.4	37.0	8	1	AAH58041	3'-primer used for
273	7.4	37.0	8	1	AAH58041	3'-primer used for
274	7.4	37.0	8	1	AAH58041	3'-primer used for
275	7.4	37.0	8	1	AAH58041	3'-primer used for
276	7.4	37.0	8	1	AAH58041	3'-primer used for
277	7.4	37.0	8	1	AAH58041	3'-primer used for
278	7.4	37.0	8	1	AAH58041	3'-primer used for
279	7.4	37.0	8	1	AAH58041	3'-primer used for
280	7.4	37.0	8	1	AAH58041	3'-primer used for
281	7.4	37.0	8	1	AAH58041	3'-primer used for
282	7.4	37.0	8	1	AAH58041	3'-primer used for
283	7.4	37.0	8	1	AAH58041	3'-primer used for
284	7.4	37.0	8	1	AAH58041	3'-primer used for
285	7.4	37.0	8	1	AAH58041	3'-primer used for
286	7.4	37.0	8	1	AAH58041	3'-primer used for
287	7.4	37.0	8	1	AAH58041	3'-primer used for
288	7.4	37.0	8	1	AAH58041	3'-primer used for
289	7.4	37.0	8	1	AAH58041	3'-primer used for
290	7.4	37.0	8	1	AAH58041	3'-primer used for
291	7.4	37.0	8	1	AAH58041	3'-primer used for
292	7.4	37.0	8	1	AAH58041	3'-primer used for
293	7.4	37.0	8	1	AAH58041	3'-primer used for
294	7.4	37.0	8	1	AAH58041	3'-primer used for
295	7.4	37.0	8	1	AAH58041	3'-primer used for
296	7.4	37.0	8	1	AAH58041	3'-primer used for
297	7.4	37.0	8	1	AAH58041	3'-primer used for
298	7.4	37.0	8	1	AAH58041	3'-primer used for
299	7.4	37.0	8	1	AAH58041	3'-primer used for
300	7.4	37.0	8	1	AAH58041	3'-primer used for

ALIGNMENTS

RESULT 1
AA29342/c
ID AAX29342 standard; DNA; 20 BP.

10-JUN-1999 (first entry)
Chemically modified sense control probe ISIS No: 14118.

Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
hyperproliferative disease; human; ss.

Synthetic.
Homo sapiens.
WO9909214-A1.
25-FEB-1999.

XX 07-AUG-1998; 98MO-US16488.
PF 13-AUG-1997; 97US-0910629.
XX (ISIS-) ISIS PHARM INC.
XX Dean N, Gaarde WA, McKay R, Monia BP, Nero PS;
XX WPI; 1999-181060/15.
XX New antisense oligonucleotides that detect and modulate the
XX expression of Jun N-terminal kinase proteins - useful for treating
XX hyperproliferative diseases and inhibiting tumor growth in animals,
XX and for modulating protein phosphorylation by these proteins
XX Example 4; Page 92; 190pp; English.
XX The invention relates to antisense oligonucleotides that detect and
XX modulate the expression of Jun N-terminal kinase (JNK) proteins. The
XX oligonucleotides specifically hybridize to a nucleic acid encoding a
XX JNK1, JNK2 or JNK3 protein, and which modulate expression of these
XX proteins. The oligonucleotides are useful for modulating JNK protein
XX expression and cell cycle progression in cultured cells or animal cells.
XX The oligonucleotides are also useful for modulating the phosphorylation
XX of a protein that has been phosphorylated by a JNK protein, and the
XX expression of a cellular protein that promotes one or more metastatic
XX events. The oligonucleotides also form pharmaceutical compositions for
XX treating animals with a hyperproliferative disease, and for inhibiting
XX tumor growth in an animal.

SO Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCGGGCGGCGCAAGTC 20
Db 20 GTCCGGGCGGCGCAAGTC 1

RESULT 2
ID AAX29331 standard; DNA; 20 BP.

10-JUN-1999 (first entry)
JNK2-specific probe ISIS No: 12560.

Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
hyperproliferative disease; human; ss.

Synthetic.
Homo sapiens.
WO9909214-A1.
25-FEB-1999.
07-AUG-1998; 98MO-US16488.
13-AUG-1997; 97US-0910629.
(ISIS-) ISIS PHARM INC.
Dean N, Gaarde WA, McKay R, Monia BP, Nero PS;
WPI; 1999-181060/15.

PT New antisense oligonucleotides that detect and modulate the
PT expression of Jun N-terminal kinase proteins - useful for treating
PT hyperproliferative diseases and inhibiting tumor growth in animals,
PT and for modulating protein phosphorylation by these proteins
XX
PS Example 4; Page 87; 190pp; English.
XX
CC The invention relates to antisense oligonucleotides that detect and
CC modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC oligonucleotides specifically hybridize to a nucleic acid encoding a
CC JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC proteins. The oligonucleotides are useful for modulating JNK protein
CC expression and cell cycle progression in cultured cells or animal cells.
CC The oligonucleotides are also useful for modulating the phosphorylation
CC of a protein that has been phosphorylated by a JNK protein, and the
CC expression of a cellular protein that promotes one or more metastatic
CC events. The oligonucleotides also form pharmaceutical compositions for
CC treating animals with a hyperproliferative disease, and for inhibiting
CC tumor growth in an animal.
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GTCCGGGCGCAGCCAAAGTC 20
Db 1 GTCCGGGCGCAGCCAAAGTC 20
XX
RESULT 3
AAC62874
ID AAC62874 standard; DNA; 20 BP.
XX
AC AAC62874;
XX
DT 06-FEB-2001 (first entry)
XX
DE JNK antisense oligonucleotide ISIS #12560.
XX
XX Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
XX cellular hyperproliferation; Alzheimer's; Parkinson's disease;
XX amyotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
XX myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
XX diabetes; Jun N-terminal kinase; ss.
XX
OS Homo sapiens.
XX
PN WO200059549-A1.
XX
PD 12-OCT-2000.
XX
PF 04-APR-2000; 2000WO-US08880.
XX
PR 07-APR-1999; 99US-0287796.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI McKay R, Dean NM, Monia BP, Nero PS, Gaarde WA;
XX
XX WPI; 2000-638427/61.
XX
PT Novel methods for reducing apoptosis comprising contacting cells with
PT antisense oligonucleotides, useful for treating apoptotic disorders,
PT e.g. cancer -
XX
PS Claim 3; Page 133; 160pp; English.
XX
CC The present invention relates to antisense oligonucleotides
CC (AAC62844-C63000, AAA96093-A96099 and AAA07993) that hybridise
CC specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
CC protein, resulting in decrease of JNK2 expression and leading to

CC induction of apoptosis. The present sequence is one such antisense
CC oligonucleotide. The oligonucleotides of the present invention are useful
CC for treating diseases or conditions with reduced apoptosis, e.g. cancer
CC and cellular hyperproliferation. The oligonucleotides may also be used to
CC increase the stimulation of apoptotic proteins, e.g. for treating
CC Alzheimer's or Parkinson's disease, amyotrophic lateral sclerosis,
CC retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
CC obstructive jaundice, polycystic kidney and diabetes. The present
CC sequence may have a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GTCCGGGCGCAGCCAAAGTC 20
Db 1 GTCCGGGCGCAGCCAAAGTC 20
XX
RESULT 4
AAC62885/C
ID AAC62885 standard; DNA; 20 BP.
XX
AC AAC62885;
XX
DT 06-FEB-2001 (first entry)
XX
DE JNK antisense oligonucleotide ISIS #14318.
XX
XX Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
XX cellular hyperproliferation; Alzheimer's; Parkinson's disease;
XX amyotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
XX myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
XX diabetes; Jun N-terminal kinase; ss.
XX
OS Homo sapiens.
XX
PN WO200059549-A1.
XX
PD 12-OCT-2000.
XX
PF 04-APR-2000; 2000WO-US08880.
XX
PR 07-APR-1999; 99US-0287796.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI McKay R, Dean NM, Monia BP, Nero PS, Gaarde WA;
XX
XX WPI; 2000-638427/61.
XX
PT Novel methods for reducing apoptosis comprising contacting cells with
PT antisense oligonucleotides, useful for treating apoptotic disorders,
PT e.g. cancer -
XX
PS Example 4; Page 135; 160pp; English.
XX
CC The present invention relates to antisense oligonucleotides
CC (AAC62844-C63000, AAA96093-A96099 and AAA07993) that hybridise
CC specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
CC protein, resulting in decrease of JNK2 expression and leading to
CC induction of apoptosis. The present sequence is one such antisense
CC oligonucleotide. The oligonucleotides of the present invention are useful
CC for treating diseases or conditions with reduced apoptosis, e.g. cancer
CC and cellular hyperproliferation. The oligonucleotides may also be used to
CC increase the stimulation of apoptotic proteins, e.g. for treating
CC Alzheimer's or Parkinson's disease, amyotrophic lateral sclerosis,
CC retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
CC obstructive jaundice, polycystic kidney and diabetes. The present
CC sequence may have a phosphorothioate backbone.

SQ Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;
 Query Match 100.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGGCGCGCCAAAGTC 20
 20 GTCCGGGCGCGCCAAAGTC 1

DB 20 GTCCGGGCGCGCCAAAGTC 1

RESULT 5
 AAA48651
 ID AAA48651 standard; DNA; 20 BP.
 AC AAA48651;
 XX
 XX 20-SEP-2000 (first entry)
 XX
 XX Antisense oligonucleotide ISIS no.15354 to human JNK2 gene.
 DE
 XX Antisense; E-selectin; TNF alpha; cell adhesion;
 KM Tumour necrosis factor alpha; phosphorothioate; methoxyethoxy;
 KM sepsis; rheumatoid arthritis; inflammatory; immune disease;
 KM inflammatory bowel disease; allergic contact dermatitis; psoriasis;
 KM diabetes; Grave's disease; allograft rejection; cancer; antibacterial;
 KM immunosuppressive; antipsoriatic; antidiabetic; antithyroid;
 KM cytoskeletal; dermatological; antiallergic; Ha-ras; c-rat;
 KM c-Jun N-terminal kinase; JNK; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..6
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "All bases are 2'-methoxyethoxy,
 FT additionally C bases are m5c"
 FT modified_base 7..15
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate internucleotide linkage"
 FT 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "All bases are 2'-methoxyethoxy,
 FT additionally C bases are m5c"
 FT XX
 FT XX
 PN MO200034303-A1.
 XX
 XX 15-JUN-2000.
 PD
 PD 08-DEC-1999; 99WO-US28965.
 XX
 XX 10-DEC-1998; 98US-0209668.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 PA Monica BP, Xu XS;
 PI
 PI WPI; 2000-423367/36.
 DR
 DR WPI; 2000-423367/36.
 XX
 XX Modulating cell adhesion molecule expression for treating immune or
 PT inflammatory diseases involves treating cell with specific inhibitor of
 PT Tumour Necrosis Factor alpha signalling molecule
 PT
 XX
 XX
 PS Claim 36; Page 46; 100pp; English.
 XX
 XX A novel method for modulating cell adhesion molecule expression
 CC involves antisense inhibition of a tumour necrosis factor (TNF) alpha
 CC signalling molecule. In the method TNF alpha signalling molecules
 CC Ha-ras, c-rat and c-Jun N-terminal kinase (JNK)2 were inhibited by
 CC antisense oligonucleotides. In addition an antisense oligonucleotide

CC to the cell adhesion molecule E-selectin was also examined. The
 CC present sequence is the JNK2 antisense oligonucleotide. The
 CC antisense oligonucleotides used in the method contained modifications,
 CC namely phosphorothioate linkages and 2'-methoxyethoxy bases. Some C
 CC residues also had a 5-methyl modification. Inhibitors of the TNF alpha
 CC signalling molecules have antibacterial, immunosuppressive,
 CC antipsoriatic, antidiabetic, antithyroid, cytoskeletal, dermatological,
 CC antiallergic and antiinflammatory activity. The antisense inhibitors
 CC may be useful for the treatment of sepsis, rheumatoid arthritis,
 CC inflammatory, immune disease, inflammatory bowel disease, allergic
 CC contact dermatitis, psoriasis, diabetes, Grave's disease, allograft
 CC rejection and cancer.
 CC
 SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
 Query Match 100.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGGCGCGCCAAAGTC 20
 1 GTCCGGGCGCGCCAAAGTC 20

DB 1 GTCCGGGCGCGCCAAAGTC 20

RESULT 6
 AAH23754
 ID AAH23754 standard; DNA; 20 BP.
 XX
 XX AAH23754;
 AC
 XX
 XX 13-AUG-2001 (first entry)
 DT
 XX
 XX JNK1 antisense oligonucleotide, JNK2AS, (ISIS #12560).
 DE
 XX
 XX JNK; jun kinase; antisenese; cytostatic; cancer;
 KM 2'-O-methoxyethyl oligonucleotide; MOE; phosphorothioate; ss.
 KM
 XX Synthetic.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= "OTHER"
 FT /note= "This oligonucleotide is a 2'-O-methoxyethyl (MOE)
 FT chimeric antisense oligonucleotide containing five
 FT MOE/phosphodiester residues flanking a
 FT 2'-deoxynucleotide/phosphorothioate region"
 FT XX
 FT XX
 PN MO200134792-A2.
 XX
 XX 17-MAY-2001.
 PD
 PD 10-NOV-2000; 2000MO-US30869.
 XX
 XX 12-NOV-1999; 99US-0165224.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 PA Potapova O, Gorospe M, Holbrook NJ;
 PI
 PI WPI; 2001-335925/35.
 DR
 DR WPI; 2001-335925/35.
 XX
 XX Use of Jun Kinase antisense mRNA for treating cancer by administering
 PT vector comprising promoter operably linked to DNA sequence that encodes
 PT the antisense mRNA to patient diagnosed with cancer
 PT
 XX
 XX
 PS Claim 1; Page 41; 75pp; English.
 XX
 XX The present invention relates to the use of Jun Kinase (JNK) antisense
 CC oligonucleotides for treating cancer and for screening compounds that
 CC mimic or augment the effect of JNK antisense oligonucleotides treatment
 CC for cancer. The present sequence is one such JNK antisense
 CC oligonucleotide.

XX SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCGGGCCAGGCCAAAGTC 20
DB 1 GTCCGGGCCAGGCCAAAGTC 20
RESULT 7
AAAF9183
AAAF9183 standard; DNA; 20 BP.
XX AAF9183;
AC AAF9183;
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #299.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122872-A2.
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US26383.
XX
PR 25-SEP-1999; 99US-0156113.
PR 27-SEP-1999; 99US-0156135.
PR 23-AUG-2000; 2000US-0227436.
XX
PA (IOWA) UNIV IOWA RES. FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Volmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and Tg nucleic acids -
XX
PS Claim 101; Page 44; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-todent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCGGGCCAGGCCAAAGTC 20

DB 1 GTCCGGGCCAGGCCAAAGTC 20
RESULT 8
ABST7827
ID ABST7827 standard; DNA; 20 BP.
XX
AC ABST7827;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #311.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis;
KW psoriasis; diabetic retinopathy; retinopathy of prematurity;
KW macular degeneration; corneal graft rejection; neovascular glaucoma;
KW retrolental fibroplasia; rubecosis; Osler-Weber Syndrome;
KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
KW haemophilic joint; angiodioma; wound granulation;
KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US48458.
XX
PR 14-DEC-2000; 2000US-25534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/50.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least
PT one antiangiogenic nucleic acid molecule to the subject -
XX
PS Claim 2; Page 25; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule.
CC Also included is a kit comprising a first container housing the
CC antiangiogenic nucleic acids, and instructions for administering them to
CC a subject having a condition characterised by unwanted angiogenesis.
CC The method is useful for inhibiting angiogenesis associated with solid
CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid
CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
CC macular degeneration, corneal graft rejection, neovascular glaucoma,
CC retrolental fibroplasia, rubecosis, Osler-Weber Syndrome, myocardial
CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
CC joints, angiodioma, wound granulation, intestinal adhesions,
CC atherosclerosis, scleroderma and hypertrophic scars. The present
CC sequence is an antiangiogenic nucleic acid of the invention.
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCGGGCCAGGCCAAAGTC 20
DB 1 GTCCGGGCCAGGCCAAAGTC 20
RESULT 9
ABL39057
ID ABL39057 standard; DNA; 20 BP.

```

XX ABL39057;
XX
XX 16-APR-2002 (first entry)
XX
XX Immunostimulatory nucleic acid SEQ ID NO: 463.
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate backbone"
XX
XX WO200197843-A2.
XX
XX 27-DEC-2001.
XX
XX 22-JUN-2001; 2001WO-US20154.
XX
XX 22-JUN-2000; 2000US-213346P.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Weiner G, Hartmann G,
XX
XX WPI; 2002-154611/20.
XX
XX
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
XX administering immunostimulatory nucleic acids that induce expression of
XX cell surface antigens and antibodies to a subject having or at risk of
XX developing cancer -
XX
XX Disclosure; Page 212; 312pp; English.
XX
XX The present invention relates to methods for treating or preventing
XX cancer, involving administering to a subject having or at risk of
XX developing cancer immunostimulatory nucleic acids that induce expression
XX of cell surface antigens and antibodies. The methods are useful for
XX treating or preventing cancer such as basal cell carcinoma, bladder
XX cancer, bone cancer, brain and central nervous system (CNS) cancer,
XX breast cancer, cervical cancer, colon and rectum cancer, connective
XX tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
XX non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
XX cancer, stomach cancer, testicular cancer, and uterine cancer. The
XX present sequence is an immunostimulatory oligonucleotide described in
XX the exemplification of the invention.
XX
XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.1;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GTCCGGGCGGCGCAAGTC 20
XX Db 1 GTCCGGGCGGCGCAAGTC 20
XX
XX
XX RESULT 10
XX ID AAV60744 standard; DNA; 18 BP.
XX AC AAV60744;
XX XX
XX DT 08-DEC-1998 (first entry)
XX XX

```

```

DE Primer #2 for human CDK4 codons 1-163.
XX
XX PCR primer; amplification; yeast; UAS; upstream activating sequence;
XX transcription terminator; cell cycle; Upstream Activation Sequence; UAS;
XX promoter; phosphorylation; cyclin; cyclin-dependent kinase; CDK; vector;
XX cyclin kinase inhibitor; CKI; growth; wound healing; cancer therapy; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO9816660-A1.
XX
XX 23-APR-1998.
XX
XX
XX 16-OCT-1997; 97WO-US18608.
XX
XX 27-NOV-1996; 96US-0031968.
XX
XX 16-OCT-1996; 96US-0029127.
XX
XX
XX (BITT-) BITTECH INC.
XX
XX Bitter GA;
XX
XX WPI; 1998-251302/22.
XX
XX
XX Screening for agents that effect cell cycle regulatory proteins -
XX using a cell line that expresses a reporter gene in response to
XX regulation through phosphorylation by a cyclin/CDK system
XX
XX Example 4; Page 75; 93pp; English.
XX
XX Primers AAV60743-V60745 were used to PCR amplify codons 1-163 of the
XX human cyclin-dependent kinase 4 (hCDK4). The amplified product was used
XX to generate a fusion protein comprising part of the hCDK4 sequence
XX linked to codons 154-302 of the yeast PHO85 gene. The fusion protein is
XX used to screen for compounds that affect mammalian cell cycle regulatory
XX proteins. The method comprises administering a compound to a cell line
XX which contains a reporter gene linked to an Upstream Activation Sequence
XX (UAS) and a promoter, where the UAS binds a transcription control factor
XX (TCF) which is regulated through cyclin/cyclin-dependent kinase (CDK)
XX phosphorylation. Also included in the construct is an effector gene
XX providing a gene product to permit normal cyclin/CDK regulation of the
XX TCF. Expression of the reporter gene is then analysed in the cell line,
XX thereby determining whether the compound affects the normal regulation.
XX The method can be used to identify inhibitors and activators of
XX mammalian cell cycle regulatory proteins, especially cyclin kinase
XX activators of cyclins, CDKs, cyclin/CDK complexes, cyclin kinase
XX inhibitors (CKIs), and cyclin/CDK complexes. The identified agents
XX can be used for stimulating growth of cells (as in wound healing), or
XX regulating excessive cell growth and division (as in cancer therapy).
XX
XX Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 other;
XX
XX Query Match 77.0%; Score 15.4; DB 1; Length 18;
XX Best Local Similarity 94.1%; Pred. No. 10.1;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 4 CGGGCCAGGCGCAAGTC 20
XX Db 2 CTGGCCAGGCGCAAGTC 18
XX
XX
XX RESULT 11
XX ID AAA82879/c
XX XX AAA82879 standard; DNA; 19 BP.
XX AC AAA82879;
XX XX
XX DT 04-DEC-2000 (first entry)
XX XX
XX cdk4 ribozyme binding site #60.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotrophic;
XX

```

KW restenosis; ss.
XX
XX Mammalia.
XX
PN WO200032765-A2.
XX
XX 08-JUN-2000.
PD
XX
XX 06-DEC-1999; 99WO-US28772.
PF
XX 04-DEC-1998; 98US-0110954.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
PI
XX WPI; 2000-412314/35.
DR
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1 -
XX
XX
PS Disclosure; Page 53; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA88415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells.
CC The ribozyme is resistant to endonuclease activity and hence is
CC efficient in restenosis treatment.
XX
SQ Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;
Query Match 75.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GGGCAGGCCAAAGTC 20
19 GGGCAGGCCAAAGTC 5
Db
RESULT 12
AAH58041/c
ID AAH58041 standard; DNA; 19 BP.
XX
AC AAH58041;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:465.
XX
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnery;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antiisoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antiscikling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200130362-A2.
PN
XX
XX 03-MAY-2001.
PD
XX
PF 26-OCT-2000; 2000WO-US29500.

XX
PR 26-OCT-1999; 99US-0161532.
XX
XX (IMMU-) IMMUSOL INC.
PA
XX
XX Robbins JM, Tritz R;
PI
XX WPI; 2001-300427/31.
DR
XX
XX Treating proliferative skin or eye diseases and scarring, using
PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
PT matrix metalloproteinases, growth factors and cell-cycle dependent
PT kinases -
XX
XX Example 1; Page 105; 408pp; English.
XX
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiscikling,
CC ophthalmological, vulnery, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative
CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;
Query Match 75.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GGGCAGGCCAAAGTC 20
19 GGGCAGGCCAAAGTC 5
Db
RESULT 13
AAH73494/c
ID AAH73494 standard; RNA; 18 BP.
XX
AC AAH73494;
XX
DT 28-JUL-1999 (first entry)
XX
XX Mouse flk-1 VEGF receptor hairpin ribozyme substrate #41.
DE
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX
OS Mus sp.
OS
PN WO9715662-A2.
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US17480.
PF
XX 11-JAN-1996; 96US-0584040.
PR
XX 26-OCT-1995; 95US-0005974.

XX (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D,
XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX Claim 4; Page 152; 218pp; English.
XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SO Sequence 18 BP; 1 A; 6 C; 7 G; 4 U; 0 other;
Query Match 74.0%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 CCGGGCCAGGCCAAGTC 20
DB 18 CCGGGCCAGGCCAAGTC 1
RESULT 14
AAX71472/c
ID AAX71472 standard; RNA; 17 BP.
XX AAX71472;
AC
XX
XX 28-JUL-1999 (first entry)
DT
XX
XX Human KDR VEGF receptor hammerhead ribozyme substrate #484.
DE
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KM flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US17480.
PF
XX
XX 11-JAN-1996; 96US-0584040.
PR
XX 26-OCT-1995; 95US-0005974.
PR
XX
XX (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D,
XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient

XX Claim 4; Page 111; 218pp; English.
PS
XX
XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SO Sequence 17 BP; 0 A; 5 C; 7 G; 5 U; 0 other;
Query Match 72.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 CCGGGCCAGGCCAAG 18
DB 16 CCGGGCCAGGCCAAG 1
RESULT 15
AAX74911/c
ID AAX74911 standard; RNA; 17 BP.
XX AAX74911;
AC
XX
XX 28-JUL-1999 (first entry)
DT
XX
XX Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #439.
DE
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KM flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
XX Mus sp.
OS
XX
XX WO9715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US17480.
PF
XX
XX 11-JAN-1996; 96US-0584040.
PR
XX 26-OCT-1995; 95US-0005974.
PR
XX
XX (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D,
XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX Claim 4; Page 168; 218pp; English.
XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression

CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 17 BP; 1 A; 5 C; 6 G; 5 U; 0 other;

Query Match 70.0%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCCAGGCCCAAGTC 20
17 GCCAGGCCCAAGTC 4

RESULT 16
AAX69246/c
ID AAX69246 standard; RNA; 17 BP.

XX AAX69246;

XX 28-JUL-1999 (first entry)

XX Human flt1 VEGF receptor hammethead ribozyme substrate #541.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX flk-1; KDR; hammethead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.

XX Homo sapiens.

XX MO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US17480.

XX 11-JAN-1996; 96US-0584040.

XX 26-OCT-1995; 95US-0005974.

XX (CHIR) CHIRON CORP.
XX (RIBO-) RIBOZYME PHARM INC.

XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX psoriasis, rheumatoid arthritis, etc., in a human patient

XX Claim 4; Page 63; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX be treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention.

XX Sequence 17 BP; 1 A; 5 C; 6 G; 5 U; 0 other;

Query Match 67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGCCCAA 17
|||||

DB 15 CCGGGCCAGGCCCAA 1

RESULT 17

XX AAD03853 standard; DNA; 17 BP.

XX AAD03853;

XX 02-JUL-2001 (first entry)

XX Human cell cycle checkpoint protein, hchk1 DNA amplifying PCR primer #2.

XX Human, cell cycle checkpoint; chk1; tumour; malignancy;

XX cell growth inhibitor; development deficiency; PCR primer;

XX DNA damage; kinase; ss.

XX Homo sapiens.

XX US6218109-B1.

XX 17-APR-2001.

XX 05-SEP-1997; 97US-0924183.

XX 05-SEP-1997; 97US-0924183.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Elledge SJ, Sanchez Y;

XX WPI; 2001-289827/30.

XX New Chk1 proteins and gene sequences encoding the proteins useful as
XX probes for a portion of the chromosome associated with tumors and other
XX malignancies, growth and/or development deficiencies -
XX Claim 17; Column 24; 37pp; English.

XX The present sequence is a degenerate PCR primer used for amplifying the
XX human cell cycle checkpoint protein, hchk1 DNA. The cell cycle
XX checkpoints are regulatory pathways that control the order and timing of
XX cell cycle transitions, and ensure that critical events such as DNA
XX replication and chromosome segregation are completed with high fidelity.
XX The chk1 protein controls cell cycle in response to DNA damage. It
XX functions as kinase and phosphorylates the key regulators of Cdk tyrosine
XX phosphorylation. The checkpoint gene sequences are used as probes for a
XX portion of the chromosome associated with tumors and other malignancies,
XX as well as growth and/or development deficiencies. The chk1 proteins are
XX useful for generating specific antibodies and for inhibiting growth of
XX cells.

XX Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;

Query Match 67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCCAGGCCCAAGTC 20
3 GGACAGGCCCAAGTC 17

RESULT 18

XX AAS18424 standard; DNA; 17 BP.

XX AAS18424;

XX 12-MAR-2002 (first entry)

XX Degenerate PCR primer #2 used to amplify DNA encoding human chk1.

XX

KW Human; checkpoint protein; hchk1; DNA damage; chromosome 11q24;
 KW cell cycle checkpoint pathway; inhibition of cell growth; tumour;
 KW malignancy; growth deficiency; development deficiency; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6307015-B1.
 XX
 PD 23-OCT-2001.
 XX
 PF 12-JAN-2000; 2000US-0488364.
 XX
 PR 05-SEP-1997; 97US-0924183.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Elledge SJ, Sanchez Y;
 XX
 DR WPI; 2002-040207/05.
 XX
 PT New mammalian checkpoint protein and gene, for generating specific
 PT antibodies or for inhibiting the growth of cells; and for use as a
 PT probe for a portion of a chromosome associated with tumours or
 PT malignancies -
 PS
 PS Example 1; Column 24; 39pp; English.
 XX
 CC The present invention relates to the isolation of human and mouse
 CC checkpoint (chk1) proteins and the nucleic acid sequences encoding them.
 CC Human chk1 (hchk1) maps to chromosome 11q24. Chk1 is involved in
 CC cellular responses to DNA damage, in the cell cycle checkpoint pathway.
 CC The protein is useful for generating specific antibodies and for
 CC inhibiting the growth of cells. The nucleotide sequence encoding the
 CC protein may be used as a probe for a portion of the chromosome
 CC associated with tumours and other malignancies, as well as growth and/or
 CC development deficiencies. The present sequence represents a degenerate
 CC PCR primer used to amplify DNA encoding human chk1 protein.
 CC
 SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;
 XX
 QY Query Match 67.0%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 25;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 6 GGCCAGGCCCAAGTC 20
 3 GGACAGGCCCAAGTC 17
 XX
 RESULT 19
 ABX16354
 ID ABX16354 standard; DNA; 17 BP.
 XX
 AC ABX16354;
 XX
 DT 08-APR-2003 (first entry)
 XX
 DE Human checkpoint gene Chk1 PCR primer #2.
 XX
 KW Human; checkpoint; chk1; anti-Chk1 antibody; tumour;
 KW PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002156247-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 12-DEC-2001; 2001US-0020038.
 XX
 PR 12-JAN-2000; 2000US-0488364.
 XX
 PA (ELLE/) ELLEDGE S J.

PA (SANC/) SANCHEZ Y.
 XX
 PI Elledge SJ, Sanchez Y;
 XX
 DR WPI; 2003-182651/18.
 XX
 PT New anti-Chk1 antibody, that may be a monoclonal or polyclonal
 PT antibody, useful for detecting a Chk1 protein that is associated with a
 PT tumor -
 PS
 PS Example 1; Page 13; 28pp; English.
 XX
 CC The invention describes an anti-Chk1 antibody capable of specifically
 CC binding to an antigenic determinant on the proteins encoded by a
 CC sequence comprising 476 (3 sequences), 479, 496 or 513 amino acids.
 CC A new method is used to produce the antibody, which is useful for
 CC detecting a Chk1 protein that is associated with a tumour. This
 CC sequence represents a PCR primer used to isolate DNA encoding the
 CC human checkpoint protein Chk1.
 CC
 SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;
 XX
 QY Query Match 67.0%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 25;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 6 GGCCAGGCCCAAGTC 20
 3 GGACAGGCCCAAGTC 17
 XX
 RESULT 20
 AAX74910/C
 ID AAX74910 standard; RNA; 17 BP.
 XX
 AC AAX74910;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #438.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Mus sp.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US17480.
 XX
 PR 11-JAN-1996; 96US-0584040.
 PR 26-OCT-1995; 95US-0005974.
 XX
 PA (CHIR) CHIRON CORP.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 XX
 DR WPI; 1997-259017/23.
 XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 PS Claim 4; Page 168; 218pp; English.
 CC The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more

CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 U; 0 other;
Query Match 65.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CCAGGCCCAAGTC 20
DB 17 CCAGGCCCAAGTC 5
RESULT 21
AAX73045/c
ID AAX73045 standard; RNA; 17 BP.
XX
AC AAX73045;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #478.
XX
KM Vascular endothelial growth factor receptor; flt-1;
KM flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US17480.
XX
PR 11-JAN-1996; 96US-0584040.
XX 26-OCT-1995; 95US-0005974.
PA (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 4; Page 138; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 17 BP; 0 A; 6 C; 7 G; 4 U; 0 other;

Query Match 64.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 35;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 CCGGGCCAGCCCAAG 18
DB 16 CCGGGCCCAAGCCGAAG 1
RESULT 22
AAS19798
ID AAS19798 standard; DNA; 15 BP.
XX
AC AAS19798;
XX
DT 08-MAY-2002 (first entry)
XX
DE ASO primer #56 to detect human RANGAP1 gene polymorphisms.
XX
KM Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping
KM chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
KM cancer; irregular cell cycle associated disorder; ASO; primer; ss.
KM allele-specific oligonucleotide.
XX
OS Homo sapiens.
XX
PN WO200179240-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12455.
XX
PR 17-APR-2000; 2000US-198072P.
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshy B;
XX
DR WPI; 2002-075068/10.
XX
PT Genotyping human Ran GTPase activating protein 1 gene of individual for
PT determining haplotype of individual, involves determining identity of
PT nucleotide pair at specific polymorphic sites for two copies of the
PT gene
XX
PS Claim 15; Page 15; 148pp; English.
XX
CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC genotyping the RANGAP1 gene. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC primer-extension oligonucleotides for detecting the RANGAP1 gene
CC polymorphisms. The oligonucleotides and screened compounds are useful for
CC treatment of diseases associated with RANGAP1 activity, such as
CC cancer and other disorders associated with an irregular cell cycle.
CC AAS19743-AAS19820 represent ASO primers for detecting human RANGAP1
CC gene polymorphisms.
XX
SQ Sequence 15 BP; 3 A; 6 C; 5 G; 0 U; 1 other;
Query Match 57.0%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 CCGGGCCAGCCCA 15
DB 1 CCGGGCCAGGACA 13
RESULT 23
AAT76461/c
ID AAT76461 standard; DNA; 14 BP.

XX AAT76461;
 AC
 XX
 DT 16-SEP-1997 (first entry)
 XX
 XX Chymase antisense oligonucleotide.
 DE
 XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
 KM chronic obstructive pulmonary disease; bronchitis; ss.
 XX
 OS Synthetic.
 XX
 PN WO9640162-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US09306.
 XX
 PR 07-JUN-1995; 95US-0474497.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PI Metzger WJ, Nyce JW;
 DR WPI; 1997-051871/05.
 XX
 PT Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligonucleotide to airway epithelium of
 PT subject
 PS Example 5; Page 41; 71pp; English.
 XX
 CC A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide specific
 CC for chymase. The method can be used to treat airway diseases such as
 CC cystic fibrosis, asthma, chronic obstructive pulmonary disease,
 CC bronchitis and other airway diseases characterised by an inflammatory
 CC response. By eliminating adenosine from the antisense ON, its liberation
 CC upon antisense degradation is prevented, thereby preventing adenosine-
 CC induced bronchoconstriction in patients with hyper-reactive airways.
 CC
 SQ Sequence 14 BP; 0 A; 8 C; 3 G; 3 T; 0 other;
 XX
 SO
 Query Match 54.0%; Score 10.8; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 59;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 5 GGGCCAGGCCAAG 18
 Db 14 GGGCCAGGCCAAG 1

RESULT 24
 AAX54253/C
 ID AAX54253 standard; DNA; 14 BP.
 XX
 AC AAX54253;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 XX Chymase antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;
 KM impaired respiration; inflammation; lung disease;
 KM pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KM acute asthma; allergy; asthma; impeded respiration;
 KM respiratory distress syndrome; pain; cystic fibrosis;
 KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;

KM prostate cancer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9913886-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19419.
 XX
 PR 09-JUN-1998; 98US-0093972.
 PR 17-SEP-1997; 97US-0059160.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PI Nyce JW;
 DR WPI; 1999-229400/19.
 XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 PS Disclosure; Page 60; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, coding and
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences AAX5272-74. These multiple target
 CC oligonucleotides (specifically AAX5180-271) can be used for the
 CC antisense treatment of diseases and conditions. Typical diseases and
 CC conditions are those associated with impaired respiration and
 CC inflammation, including lung diseases, pulmonary vasoconstriction,
 CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
 CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
 CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
 CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
 CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
 CC hepatic metastases, as well as all types of cancers which may metastasize
 CC or have metastasized to the lungs, including breast and prostate cancer.
 CC
 SQ Sequence 14 BP; 0 A; 8 C; 3 G; 3 T; 0 other;
 XX
 SO

Query Match 54.0%; Score 10.8; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 59;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 5 GGGCCAGGCCAAG 18
 Db 14 GGGCCAGGCCAAG 1

RESULT 25
 AAF19819/C
 ID AAF19819 standard; DNA; 14 BP.
 XX
 AC AAF19819;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 XX Human chymase polynucleotide fragment #1386.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammation;
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;


```

RESULT 27
AA241523
ID AA241523 standard; DNA; 12 BP.
XX
AC AA241523;
XX
DT 19-JAN-2000 (first entry)
XX
DE Microbe detection in organic waste arbitrarily primed PCR primer #100.
XX
KW Microbe; detection; organic waste; arbitrarily primer PCR;
KM random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
OS Synthetic.
XX
PN JP1276176-A.
XX
PD 12-OCT-1999.
XX
PF 31-MAR-1998; 98JP-0087652.
XX
PR 31-MAR-1998; 98JP-0087652.
XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
(NORI-) ZH NORIN SUISAN SENTAN GIUTSU SANGYO.
XX
DR WPI; 1999-626940/54.
XX
XX
PT Amplification of a DNA fragment - in order to establish the state of
existence of a microbe
XX
PS Claim 1; Page 9; 40pp; Japanese.
XX
CC A method has been developed for the amplification of a DNA fragment in
which amplification is carried out on the DNA fragments of a number of
different DNAs. The method comprises a PCR reaction repeatedly carrying
out a heat-denaturing step, a primer annealing step and a polymerase
extending step, to amplify the DNA fragments of a plural of different
DNAs. The method can detect the existence of a microbe in organic waste.
CC AA241424 to AA241639 represent PCR primers used in random amplified
CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
CC organic waste.
XX
SQ Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 other;

Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 50;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CAGGCCCAAGTC 20
    ||||| |||||
DB 1 CAGGCCCAAGTC 12

RESULT 28
AA241739
ID AA241739 standard; DNA; 12 BP.
XX
AC AA241739;
XX
DT 20-MAR-2003 (updated)
21-JAN-2000 (first entry)
XX
DE Organic material detecting primer 100.
XX
KW Amplification; polymerase chain reaction; PCR; microorganism; compost;
KM detection; pollutant; soil; food; agricultural chemical; polymer;
XX organochlorine; primer; ss.
XX
OS Synthetic.
XX
PN DE19914461-A1.

```

```

XX
PD 21-OCT-1999.
XX
PF 30-MAR-1999; 99DE-1014461.
XX
PR 31-MAR-1998; 98JP-0087651.
XX
PR 16-MAR-1999; 99JP-0069694.
XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
(NORI-) SOC TECHNO-INNOVATION AGRIC FORESTRY & FI.
XX
PI Inoue T;
XX
DR WPI; 1999-592157/51.
XX
XX
PT Novel polymerase chain reaction method, for differentiating between
microorganisms and for detecting contaminants
XX
PS Example 1; Page 19; 78pp; German.
XX
CC This invention describes a novel method for the amplification of DNA
comprising (i) preparing many primers (P) with different probabilities
of amplification and (ii) simultaneous polymerase chain reaction (PCR)
of many different DNA using these primers. The method is used (i) to
differentiate between different microorganisms in a mixed population
and (ii) to determine presence/absence of an impurity (pollutant), or
its concentration, in e.g. soil, foods, compost etc., typically metals,
agricultural chemicals, polymers, organochlorine compounds etc. A
particular use is monitoring composting of organic material.
CC Amplification with many primers produces a lot of information, so
CC reliability of the test is improved, and many samples may be tested
quickly. AA241640-241855 represent the primers described in the method
of the invention.
CC (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 other;

Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 50;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CAGGCCCAAGTC 20
    ||||| |||||
DB 1 CAGGCCCAAGTC 12

RESULT 29
AAC97874
ID AAC97874 standard; DNA; 12 BP.
XX
AC AAC97874;
XX
DT 28-FEB-2001 (first entry)
XX
DE Primer used to illustrate DNA amplification method SEQ ID 100.
XX
KW Primer; amplification; selective; ss.
XX
OS Synthetic.
XX
PN JP2000270867-A.
XX
PD 03-OCT-2000.
XX
PF 19-MAR-1999; 99JP-0076844.
XX
PR 19-MAR-1999; 99JP-0076844.
XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
(NORI-) ZH NORIN SUISAN SENTAN GIUTSU SANGYO.
XX
XX
DR WPI; 2001-011047/02.

```

PT Amplification of a DNA fragment and its apparatus -
XX
PS Example 1; Page 9; 32pp; Japanese.
XX
CC This invention relates to a method for amplifying a DNA fragment. The
CC method comprises successive repetitions of heat-denaturing, annealing of
CC a primer and an extending step using a DNA polymerase. The method makes
CC use of a cDNA pool in which the primer is one primer or a pair of primer
CC sets and has an amplification probability which allows it to amplify a
CC DNA fragment from a limited number of the cDNAs among the DNA pool
CC (where the limited number is in the range of 1 to 25). Also included in
CC the invention are apparatus used for carrying out the method, a primer
CC and a DNA polymerase and a kit used for amplifying a DNA fragment. The
CC method can be used to amplify a limited number of cDNAs from a pool in
CC which a wide variety of cDNAs are present. Oligonucleotides AAC97775 -
CC AAC97990 represent primers used in an example illustrating the method of
CC the invention.
XX
SQ Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 other;
XX
Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 50;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 CAGGCCCAAGTC 20
1 CAGGCCCAAGTC 12
Db 1 CAGGCCCAAGTC 12
RESULT 30
AAZ81584/c
ID AAZ81584 standard; DNA; 10 BP.
XX
AC AAZ81584;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #818.
XX
KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KM non-metastatic breast tumour tissue; gene therapy; anticancer;
KM antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 80; 21pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast

CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides or as
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;
XX
Query Match 50.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TCCGGGCGAG 11
10 TCCGGGCGAG 1
Db 10 TCCGGGCGAG 1
RESULT 31
AAZ86676/c
ID AAZ86676 standard; DNA; 10 BP.
XX
AC AAZ86676;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5910.
XX
KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KM non-metastatic breast tumour tissue; gene therapy; anticancer;
KM antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 214; 21pp; English.
XX

CC AA280767 to AA283941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis,
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC Diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.

SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 other;

Query Match 50.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GCCAGGCCAA 16
 |||||
 10 GCCAGGCCAA 1

Db

RESULT 32
 AAH64570/c
 ID AAH64570 standard; cDNA; 10 BP.
 XX
 AC AAH64570;
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1410.
 XX
 KM Human; transcriptome; gene expression pattern; cancer; drug screening;
 XX cancer diagnosis; cell specific gene expression; ss.
 XX Homo sapiens.
 XX OS
 XX PN WO200138577-A2.
 XX PD 31-MAY-2001.
 XX PF 21-NOV-2000; 2000WO-US31922.
 XX PR 24-NOV-1999; 99US-0448480.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Velulescu VE, Vogelstein B, Kinzler KW;
 XX WPI; 2001-367706/38.
 XX
 PT New isolated polynucleotides, useful for identifying specific cell
 PT type, such as cancer cell, comprises transcriptomes expressed in
 PT particular cell types -
 XX
 PS Claim 13; Page 71; 94pp; English.
 XX
 CC The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences
 CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
 CC in the invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of
 CC the transcriptomes described in the exemplification of the invention.

CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of
 CC the transcriptomes described in the exemplification of the invention.

SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

Query Match 50.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TCCGGGCCAG 11
 |||||
 10 TCCGGGCCAG 1

Db

RESULT 33
 AAH64571/c
 ID AAH64571 standard; cDNA; 10 BP.
 XX
 AC AAH64571;
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1411.
 XX
 KM Human; transcriptome; gene expression pattern; cancer; drug screening;
 XX cancer diagnosis; cell specific gene expression; ss.
 XX Homo sapiens.
 XX OS
 XX PN WO200138577-A2.
 XX PD 31-MAY-2001.
 XX PF 21-NOV-2000; 2000WO-US31922.
 XX PR 24-NOV-1999; 99US-0448480.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Velulescu VE, Vogelstein B, Kinzler KW;
 XX WPI; 2001-367706/38.
 XX
 PT New isolated polynucleotides, useful for identifying specific cell
 PT type, such as cancer cell, comprises transcriptomes expressed in
 PT particular cell types -
 XX
 PS Claim 13; Page 71; 94pp; English.
 XX
 CC The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences
 CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
 CC in the invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of
 CC the transcriptomes described in the exemplification of the invention.

SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

Query Match 50.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TCCGGGCCAG 11
 |||||
 10 TCCGGGCCAG 1

Db

RESULT 34
 ABZ72939
 ID ABZ72939 standard; RNA; 12 BP.

XX AC AB272939;
 XX DT 09-APR-2003 (first entry)
 XX DE Rod opsin hammerhead ribozyme oligonucleotide.
 XX KM Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease;
 XX KM target; ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
 XX KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
 XX KM blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN W0200288320-A2.
 XX PD 07-NOV-2002.
 XX PF 01-MAY-2002; 2002MO-US13679.
 XX PR 01-MAY-2001; 2001US-0847601.
 XX PA (UYFL) UNIV FLORIDA.
 XX PI Lewin AS, Shaw LC, Grant MB;
 XX DR WPI; 2003-111880/10.
 XX XX A recombinant adeno-associated virus-vectored ribozyme composition,
 PT useful for treating a disease or dysfunction of the mammalian eye e.g.
 PT retinal disease, e.g. diabetic retinopathy or age-related macular
 PT degeneration -
 XX PS Example 5; Page 73; 115pp; English.
 XX XX The present invention describes a recombinant adeno-associated virus
 CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
 CC first ribozyme that specifically cleaves an mRNA encoding a protein,
 CC polypeptide, or peptide selected from the group of rod opsin, inos,
 CC RGS/peripherin, VEGFR1, VEGFR2, adenosine A-28 receptor, IGF-1, integrin
 CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
 CC vector comprising a polynucleotide encoding the ribozyme, where the
 CC polynucleotide operably positioned downstream of at least a first
 CC promoter that directs expression of the polynucleotide in a selected
 CC mammalian cell transformed with the vector; (c) a viral particle
 CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
 CC comprising the ribozyme or the polynucleotide; or (e) a host cell
 CC comprising the ribozyme or the polynucleotide. Also described is a method
 CC for decreasing the amount of mRNA encoding a selected polypeptide in a
 CC retinal cell of a mammalian eye, comprising providing to the eye the
 CC composition described above, and for a time effective to specifically
 CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
 CC be used in gene therapy. (I) can be used for treating a disease or
 CC dysfunction of the mammalian eye, such as a retinal disease or retinal
 CC dysfunction, (diabetic) retinopathy, or (age-related) macular
 CC degeneration. (I) is also useful for manufacturing a medicament for
 CC treating the diseases mentioned above, including autosomal dominant
 CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
 CC for treating, decreasing the severity, or ameliorating the symptoms of a
 CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
 CC blindness, a reduction in central or peripheral vision, or a reduction in
 CC total vision. AB272763 to AB272953 represent sequences used in the
 CC exemplification of the present invention.
 XX XX
 XX S0 Sequence 12 BP; 3 A; 4 C; 4 G; 1 U; 0 other;
 XX
 XX Query Match 50.0%; Score 10; DB 1; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 61;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 6 GGCCAGGCCCA 15
 XX |||||||||

DB 3 GGCCAGGCCCA 12
 RESULT 35
 ID AAV63772 standard; DNA; 13 BP.
 XX AC AAV63772;
 XX DT 26-APR-1999 (first entry)
 XX DE Human JAGGED1 exon 23 mutation associated with Alagille Syndrome.
 XX KM JAGGED1; JAGGED1; hJAGGED1; human; notch ligand; stem cell;
 XX KM progenitor cell; haematopoiesis; cell differentiation; mutant;
 XX KM Alagille syndrome; leukaemia; lymphoma; diagnosis; therapy; ss.
 XX OS Homo sapiens.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT mutation 7..11
 XX FT /tag= a
 XX FT /note= "5-base insertion"
 XX PN W09858958-A2.
 XX PD 30-DEC-1998.
 XX PF 25-JUN-1998; 98WO-US13207.
 XX PR 25-JUN-1997; 97US-0882046.
 XX PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
 XX PA (UNIM) UNIV WASHINGTON.
 XX PI Hood L, Krantz ID, Li L, Spinner NB;
 XX DR WPI; 1999-081220/07.
 XX XX New Jagged peptides for inhibiting differentiation of progenitor
 PT cells - also used for maintaining these cells in undifferentiated
 PT state, e.g. for haematopoietic reconstitution
 XX PS Example 5; Fig 8; 101pp; English.
 XX XX This nucleotide corresponds to a portion of exon 23 of the human
 CC JAGGED1 gene that is mutated in affected individuals of an
 CC Alagille Syndrome (AS) family. The mutation involves insertion of
 CC 'GTGCG' residues at a position corresponding to nucleotide 3102
 CC (see AAV63773) of an hJAGGED1 cDNA (see AAV63753). The mutation causes
 CC a frameshift that results in premature truncation of the gene
 CC product (see AAV87904). It was detected by heteroduplex mobility
 CC analysis (see AAV63767-68 and AAV84310-19). hJAGGED1 (see also
 CC AAV87894) is a novel Notch ligand capable of inhibiting the
 CC differentiation of haematopoietic progenitor cells. Methods are provided
 CC for the diagnosis of AS based on detection of disease-associated
 CC mutations or truncated hJAGGED1 gene products.
 XX XX
 XX S0 Sequence 13 BP; 0 A; 4 C; 6 G; 3 T; 0 other;
 XX
 XX Query Match 49.0%; Score 9.8; DB 1; Length 13;
 XX Best Local Similarity 84.6%; Pred. No. 81;
 XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX 5 GGCCAGGCCCAA 17
 XX |||||||||
 XX DB 13 GGCCAGGCCACA 1
 XX
 XX RESULT 36
 XX AAA04950/c
 XX ID AAA04950 standard; DNA; 13 BP.
 XX

AC AAA04950;
XX
DT 18-MAY-2000 (first entry)
XX
DE Tenascin-C phosphorothioate antisense oligonucleotide SEQ ID NO:239.
XX
XX
KM Human; Tenascin-C; extracellular matrix protein; phosphorothioate;
KM antisense oligonucleotide; inhibition; exon deletion; therapy;
KM cellular development; differentiation; translation; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200006775-A1.
XX
PD 10-FEB-2000.
XX
PF 23-JUL-1999; 99WO-US16632.
XX
PR 27-JUL-1998; 98US-0094255.
XX
PI (UYVI-) UNIV VIRGINIA COMMONWEALTH.
XX
PI Fillmore H, Broadus WC, Gillies GT, Conrad WS;
XX
DR WPI; 2000-183137/16.
XX
PT Preparing antisense oligodeoxynucleotides (ODNs) and long antisense RNA
PT sequences useful for blocking translation of a specific isoform of
PT Tenascin-C protein -
XX
XX
PS Claim 23; Page 102; 177pp; English.
XX
XX The present invention describes a method for preparing an antisense
CC oligodeoxynucleotide (ODN) sequence for blocking translation of a
CC specific protein isoform that can be expressed as a number of different
CC isoforms. AAA04712 to AAA05243 represent specifically claimed
CC phosphorothioate antisense ODNs for blocking translation of Tenascin-C
CC using the method of the invention. The method is useful for preparing
CC an ODN sequence for blocking translation of a specific isoform of
CC Tenascin-C protein. The method is also useful for blocking translation
CC of a specific family of isoforms of a protein. The method can also be
CC performed by producing a long antisense expression vector encoding a
CC long antisense RNA sequence for blocking translation of a specific
CC protein isoform. The ODNs and long antisense constructs are useful in
CC designing models for studying cellular development and differentiation.
CC The method permits selective inhibition of the translation of protein
CC isoforms, which occur as a result of alternative splicing. AAA05244
CC represent an oligonucleotide from the present invention, which is given
CC in the sequence listing but not mentioned further within the
CC specification.
XX
SQ Sequence 13 BP; 0 A; 5 C; 4 G; 4 T; 0 other;
XX
QY Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 81;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Db 6 GGGCAGGCCCAAG 18
13 GGGCAAGCCGAG 1

RESULT 37
AAA05213/c
ID AAA05213 standard; DNA; 13 BP.
XX
AC AAA05213;
XX
DT 18-MAY-2000 (first entry)
XX
DE Tenascin-C phosphorothioate antisense oligonucleotide SEQ ID NO:502.
XX

KM Human; Tenascin-C; extracellular matrix protein; phosphorothioate;
KM antisense oligonucleotide; inhibition; exon deletion; therapy;
KM cellular development; differentiation; translation; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200006775-A1.
XX
PD 10-FEB-2000.
XX
PF 23-JUL-1999; 99WO-US16632.
XX
PR 27-JUL-1998; 98US-0094255.
XX
PI (UYVI-) UNIV VIRGINIA COMMONWEALTH.
XX
PI Fillmore H, Broadus WC, Gillies GT, Conrad WS;
XX
DR WPI; 2000-183137/16.
XX
PT Preparing antisense oligodeoxynucleotides (ODNs) and long antisense RNA
PT sequences useful for blocking translation of a specific isoform of
PT Tenascin-C protein -
XX
XX
PS Claim 23; Page 167; 177pp; English.
XX
XX The present invention describes a method for preparing an antisense
CC oligodeoxynucleotide (ODN) sequence for blocking translation of a
CC specific protein isoform that can be expressed as a number of different
CC isoforms. AAA04712 to AAA05243 represent specifically claimed
CC phosphorothioate antisense ODNs for blocking translation of Tenascin-C
CC using the method of the invention. The method is useful for preparing
CC an ODN sequence for blocking translation of a specific isoform of
CC Tenascin-C protein. The method is also useful for blocking translation
CC of a specific family of isoforms of a protein. The method can also be
CC performed by producing a long antisense expression vector encoding a
CC long antisense RNA sequence for blocking translation of a specific
CC protein isoform. The ODNs and long antisense constructs are useful in
CC designing models for studying cellular development and differentiation.
CC The method permits selective inhibition of the translation of protein
CC isoforms, which occur as a result of alternative splicing. AAA05244
CC represent an oligonucleotide from the present invention, which is given
CC in the sequence listing but not mentioned further within the
CC specification.
XX
SQ Sequence 13 BP; 0 A; 5 C; 4 G; 4 T; 0 other;
XX
QY Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 81;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Db 6 GGGCAGGCCCAAG 18
13 GGGCAAGCCGAG 1

RESULT 38
ABC48592/c
ID ABC48592 standard; DNA; 13 BP.
XX
AC ABC48592;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 48609 for detecting SNP TSC0013829.
XX
XX
XX SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX

PN WO200177384-A2.
XX
PT 18-OCT-2001.
XX
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
XX
PS Claim 1; SEQ ID 48609; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 1 A; 1 C; 6 G; 5 T; 0 other;
XX
Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 81;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 8 CCAGGCCAAAGTC 20
Db 13 CCAGGCCAAATC 1
XX
RESULT 39
ABC48593
ID ABC48593 standard; DNA; 13 BP.
XX
AC ABC48593;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 48610 for detecting SNP TSC0013829.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.

XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
XX
PS Claim 1; SEQ ID 48610; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 5 A; 6 C; 1 G; 1 T; 0 other;
XX
Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 81;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 8 CCAGGCCAAAGTC 20
Db 1 CCAGGCCAAATC 13
XX
RESULT 40
AAZ19014
ID AAZ19014 standard; DNA; 11 BP.
XX
AC AAZ19014;
XX
XX 22-OCT-1999 (first entry)
XX
DE Murine MRL SAGE tag 3516811.
XX
XX Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
OS Mus sp.
XX
XX WO941364-A2.
XX
PN WO941364-A2.
XX
XX 19-AUG-1999.
XX
PD 12-FEB-1999; 99WO-US02962.
XX
PF 28-SEP-1998; 98US-0102051.
XX
PR 13-FEB-1998; 98US-0074737.
XX
PR 26-AUG-1998; 98US-0097937.
XX
XX (WIST-) WISTAR INST.
XX
XX Heber-Katz E;
XX
XX WPI; 1999-494533/41.
XX
DR New mammalian model for enhanced wound healing - useful for
XX identifying enhanced wound healing genes
XX
PT Claim 13; Page 74; 136pp; English.
XX
PS
XX
XX This invention describes a novel non-MRL healer mouse (M) having at
CC least one quantitative trait locus selected from those given in the
CC specification, exhibiting an enhanced healing response to a wound
CC compared to mice (m) without the locus. The invention describes a novel
CC method of identifying a gene involved in enhanced wound healing by

CC identifying DNA microsatellite markers which can distinguish healer mice
CC from non-healer mice and identifying microsatellite markers which
CC segregate with enhanced wound healing in progeny of the mice, where a
CC chromosomal locus containing at least one enhanced wound healing gene is
CC identified. A method of treating a wound in a mammal is also disclosed.
CC The new methods are useful for treating wounds, especially central and
CC peripheral nerve wound. The methods of the invention are useful for
CC restoring function after nerve injury in a mammal. (M) is useful as a
CC mammalian model of enhanced wound healing, useful for identifying genes
CC and gene products involved in enhanced wound healing, and to provide
CC methods for wound healing. AA218691-219036 represent murine SAGE tags
CC from C57BL/6 and MRL mice which are used to illustrate the method of the
CC invention.
XX
SQ Sequence 11 BP; 1 A; 3 C; 6 G; 1 T; 0 other;
Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TCCGGGCGCAGG 12
Db 1 TCCGGGCGCAGG 11
RESULT 41
AA55034/C
ID AAX55034 standard; DNA; 11 BP.
XX
AC AAX55034;
XX
DT 05-JUL-1999 (first entry)
XX
DE C/EBP-beta antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
KM pulmonary vasoconstriction; inflammation; allergic rhinitis;
KM acute asthma; allergy; asthma; impeded respiration;
KM respiratory distress syndrome; pain; cystic fibrosis;
KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KM prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US19419.
XX
PR 09-JUN-1998; 98US-0093972.
XX 17-SEP-1997; 97US-0059160.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
XX
PS Disclosure; Page 70; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding

CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences AAX55272-74. These multiple target
CC oligonucleotides (specifically AAX55180-271) can be used for the
CC antisense treatment of diseases and conditions. Typical diseases and
CC conditions are those associated with impaired respiration and
CC inflammation, including lung diseases, pulmonary vasoconstriction,
CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC hepatic metastases, as well as all types of cancers which may metastasize
CC or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;
Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 CCGGGCCAGGC 13
Db 11 CCGGGCCAGGC 11
RESULT 42
AAF20603/C
ID AAF20603 standard; DNA; 11 BP.
XX
AC AAF20603;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human C/EBP polynucleotide fragment #2170.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KM human airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 264; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense

oligonucleotides the A is replaced by a 'Universal' or alternative base. (1) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antispasmodic, hypotensive and cyostatic activities. The antisense oligonucleotides and (1) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensive, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impaired respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCGGGCCAGGC 13
Db 11 CCGGGCCAGGC 1

RESULT 43

AAC63229 standard; DNA; 11 BP.

AAC63229;

06-FEB-2001 (first entry)

Oligonucleotide #2 used in a method for primer selection.

PCR primer; nucleic acid amplification; melting temperature; T_m; ss.

Homo sapiens.

WO2000060123-A2.

12-OCT-2000.

05-APR-2000; 2000MO-US08962.

06-APR-1999; 99US-0127891.

(GENO-) GENOME TECHNOLOGIES LLC.

Senapathy P;

WPI; 2000-656235/63.

Determining T_m range for several degenerate primers with a fixed-sequence and a degenerate-sequence portion for use in polymerase chain reaction amplification by identifying a specific sequence in the nucleic acid template -
Disclosure; Fig 2; 34pp; English.

The present invention relates to a method for selecting PCR primers for nucleic acid amplification. The method comprises determining the melting temperature (T_m) range for degenerate oligonucleotide primers with a fixed-sequence portion (FS) and a degenerate-sequence portion (DS) by searching known portion of a nucleic acid template for a sequence complementary to a desired FS of a primer. Nucleotide base pairs flanking or interspersed between the sequence complementary to a DS of one of the primers are detected and T_m is calculated. The method of the present invention allows primers which produce more efficient DNA amplification to be produced. The present sequence is a primer. This sequence was used to exemplify the occurrence of a primer with a FS of 6 base pairs (CGGCCC) within a template. The remaining 5 base pairs make up the DS.

Sequence 11 BP; 1 A; 6 C; 4 G; 0 U; 0 other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CCGGCCAGGCC 14
Db 1 CCGGCCAGGCC 11

RESULT 44

AAA34481/c standard; DNA; 11 BP.

AAA34481;

28-JUL-2000 (first entry)

Human adenosine receptor related polynucleotide SEQ ID NO:2170.

Human; adenosine receptor; low adenosine antisense oligonucleotide;

phosphorothioate; impaired respiration; inflammation; allergy;

allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

antiallergic; antispasmodic; cyostatic; analgesic; impaired airway;

lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

respiratory distress syndrome; pain; cystic fibrosis; emphysema;

pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99WO-US17712.

03-AUG-1998; 98US-0095212.

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers -
Disclosure; Page 537; 1343pp; English.
The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%) which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antispasmodic, cyostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation,

CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, skin
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA3323 to AAA3392) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.

XX Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 66;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGC 13
 DB 11 CCGGGCCAGGC 1

RESULT 45

ABV62380/C
 ID ABV62380 standard; cDNA; 11 BP.

XX ABV62380;

XX 21-OCT-2002 (first entry)

DE Human skin EST 166.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KM immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KM psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

XX WO200253774-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP15179.

XX 03-JAN-2001; 2001DE-1000127.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -

PS Disclosure; Page 30; 1345pp; German.

CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or

CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhoea; lupus erythematosus; the
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.

XX Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 66;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGC 13
 DB 11 CCGGGCCAGGC 1

RESULT 46

ABV66640/C
 ID ABV66640 standard; cDNA; 11 BP.

XX ABV66640;

XX 21-OCT-2002 (first entry)

DE Human skin EST 4426.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KM immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KM psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

XX WO200253774-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP15179.

XX 03-JAN-2001; 2001DE-1000127.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -

PS Disclosure; Page 147; 1345pp; German.

CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhoea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.

XX Sequence 11 BP; 0 A; 2 C; 4 G; 5 T; 0 other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 66;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCCAAA 17
 DB 11 GCCAAGCCAAA 1

RESULT 47
 ABV69801/c
 ID ABV69801 standard; cDNA; 11 BP.
 XX
 AC ABV69801;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 7587.
 XX
 KM Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KM immunosuppressive; antiinflammatory; cytosolic; SAGE; neurodermatitis;
 KM psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP15179.
 XX
 PR 03-JAN-2001; 2001DE-1000127.
 XX
 PA (HENKEL) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX

PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -
 XX
 PS Claim 24; Page 240; 1345pp; German.
 XX

CC The invention relates to in vitro identification (MI) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (MI) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.
 CC
 XX
 SQ Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 66;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 CCGGGCCAGGC 13
 DB 11 CTTGGCCAGGC 1

RESULT 48
 AAX55033/c
 ID AAX55033 standard; DNA; 12 BP.
 XX
 AC AAX55033;
 XX
 DT 05-JUL-1999 (first entry)
 XX

DE C/EBP-beta antisense oligonucleotide fragment.
 XX
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 KM impaired respiration; inflammation; lung disease;
 KM pulmonary vasocostriction; inflammation; allergic rhinitis;
 KM acute asthma; allergy; asthma; impeded respiration;
 KM respiratory distress syndrome; pain; cystic fibrosis;
 KM pulmonary hypertension; pulmonary vasocostriction; emphysema;
 KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KM prostate cancer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9913886-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19419.
 XX
 PR 09-JUN-1998; 98US-0093972.
 XX
 PR 17-SEP-1997; 97US-0059160.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 1999-229400/19.
 XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasocostriction
 XX
 PS Disclosure; Page 70; 120pp; English.
 XX

CC The specification describes antisense oligonucleotides (AAX52869-X52711)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences AAX5272-74. These multiple target
 CC oligonucleotides (specifically AAX5180-271) can be used for the
 CC antisense treatment of diseases and conditions. Typical diseases and
 CC conditions are those associated with impaired respiration and
 CC inflammation, including lung diseases, pulmonary vasocostriction,
 CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
 CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
 CC pulmonary hypertension, pulmonary vasocostriction, emphysema, chronic
 CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
 CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
 CC hepatic metastases, as well as all types of cancers which may metastasize
 CC or have metastasized to the lungs, including breast and prostate cancer.
 CC
 XX
 SQ Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;

Query Match 47.0%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 82;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 CCGGGCCAGGC 13
 DB 12 CCGGGCCGGGC 2

RESULT 49
 AAF20602/c
 ID AAF20602 standard; DNA; 12 BP.
 XX
 AC AAF20602;
 XX

DT 14-MAR-2001 (first entry)
 XX Human C/EBP polynucleotide fragment #2169.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200062736-A2.
 PN
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000, 2000MO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX (NYCE/) NYCE J W.
 PI
 XX Nyce JW;
 XX
 XX MPI: 2000-679539/66.
 DR
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 XX Claim 14; Page 264; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cyostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 12 BP, 0 A, 7 C, 5 G, 0 U, 0 other;
 Query Match 47.0%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 82;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGC 13
 DB 12 CCGGGCCGGGC 2
 RESULT 50
 ID AAA34480/c
 ID AAA34480 standard; DNA; 12 BP.
 AC
 XX AAA34480;
 XX
 XX 28-JUL-2000 (first entry)
 DE
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2169.
 XX
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impeded airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200009525-A2.
 PN
 XX 24-FEB-2000.
 PD
 XX 03-AUG-1999; 99WO-US17712.
 PF
 XX 03-AUG-1999; 98US-0095212.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 XX
 XX MPI: 2000-205971/18.
 DR
 XX
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 XX PS Disclosure; Page 537; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cyostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32313 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

XX SQ Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;
 XX Query Match 47.0%; Score 9.4; DB 1; Length 12;
 XX Best Local Similarity 90.9%; Pred. No. 82;
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 CCGGGCCGAGC 13
 Db 12 CCGGGCCGAGC 2
 RESULT 51
 AAZ79191/c
 ID AAZ79191 standard; DNA: 10 BP.
 XX AAZ79191;
 AC 10-APR-2000 (first entry)
 XX
 DT Human dendritic cell SAGE tag, SEQ ID NO:1619.
 DE
 XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KM APC; monocyte-derived dendritic cell; differential gene expression;
 KW Immunostimulatory cofactor; costimulatory factor; CTL;
 KM cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX Homo sapiens.
 OS
 XX WO965924-A2.
 PN 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US13800.
 XX
 PF 19-JUN-1998; 98US-0089833.
 XX 19-JUN-1998; 98US-0089844.
 PR 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089878.
 PR 19-JUN-1998; 98US-0089991.
 PR 19-JUN-1998; 98US-0089992.
 PR 19-JUN-1998; 98US-0089993.
 PR 19-JUN-1998; 98US-0089994.
 PR 19-JUN-1998; 98US-0089997.
 PR 19-JUN-1998; 98US-0089999.
 PR 19-JUN-1998; 98US-0090000.
 PR 19-JUN-1998; 98US-0090035.
 PR 19-JUN-1998; 98US-0090036.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 PR 19-JUN-1998; 98US-0090042.
 PR 19-JUN-1998; 98US-0090043.
 PR 19-JUN-1998; 98US-0090044.
 PR 19-JUN-1998; 98US-0090045.
 PR 19-JUN-1998; 98US-0090047.
 PR 19-JUN-1998; 98US-0090048.
 PR 19-JUN-1998; 98US-0090072.
 PR 19-JUN-1998; 98US-0090076.
 PR 19-JUN-1998; 98US-0090077.
 PR 19-JUN-1998; 98US-0090078.
 PR 19-JUN-1998; 98US-0090079.
 PR 19-JUN-1998; 98US-0090080.
 PR 08-DEC-1998; 98US-0111715.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 XX Roberts BL, Shankara S;
 XX WPI, 2000-106077/09.

PT Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer -
 XX
 PS Claim 1; Page 111; 130pp; English.
 XX
 CC Sequence AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or
 CC ESTs (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can
 CC lyse the tumour cells. Immunostimulatory cofactors also being required
 CC for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen, to modulate the genotype of an APC, to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC, and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell
 CC differentially expressed genes, or of their encoded proteins, can be used
 CC to identify cells as belonging to the monocyte lineage. Cells containing
 CC these genes can be used in active immunotherapy (or to stimulate
 CC production of a population of antigen-specific effector cells) and
 CC vectors containing them are used in gene therapy. Co-administration of
 CC tumour antigens and APC-associated costimulatory factors ensures adequate
 CC antigen presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells.
 CC
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 other;
 XX
 XX Query Match 45.0%; Score 9; DB 1; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 64;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 AGGCCAAG 18
 Db 10 AGGCCAAG 2
 RESULT 52
 AAZ82328/c
 ID AAZ82328 standard; DNA: 10 BP.
 XX
 XX AAZ82328;
 AC
 XX 07-APR-2000 (first entry)
 DT
 XX Metastatic breast tumour cell upregulated transcript tag #1562.
 DE
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KM antimetastatic; vaccine; diagnosis; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO965928-A2.
 PN 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US13647.
 PF 19-JUN-1998; 98US-0089853.
 XX 19-JUN-1998; 98US-0089997.
 PR

PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
PI Roberts BL, Shankara S;
DR WPI; 2000-106079/09.
XX
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
PS Claim 1; Page 100; 219pp; English.
XX
XX
CC AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines, for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;
XX
Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GGCCAGGCC 14
Db 9 GGCCAGGCC 1
XX
RESULT 53
AA285483
ID AA285483 standard; DNA; 10 BP.
XX
AC AA285483;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4717.
XX
KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KM non-metastatic breast tumour tissue; gene therapy; anticancer;
KM anti-metastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN MO965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99MO-US13647.
XX

PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
PI Roberts BL, Shankara S;
DR WPI; 2000-106079/09.
XX
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
PS Claim 1; Page 185; 219pp; English.
XX
XX
CC AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines, for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 4 A; 2 C; 4 G; 0 U; 0 other;
XX
Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 AGGCCAAG 18
Db 2 AGGCCAAG 10
XX
RESULT 54
AA286477/c
ID AA286477 standard; DNA; 10 BP.
XX
AC AA286477;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5711.
XX
KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KM non-metastatic breast tumour tissue; gene therapy; anticancer;
KM anti-metastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN MO965928-A2.
XX
PD 23-DEC-1999.
XX

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PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 209; 219pp; English.
XX
CC AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells);
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines, for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 other;
XX
Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GGCCCAAGT 19
Db 10 GGCCCAAGT 2
XX
RESULT 55
AAZ86559/c
ID AAZ86559 standard; DNA; 10 BP.
XX
AC AAZ86559;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5793.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO965928-A2.
XX

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PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 211; 219pp; English.
XX
CC AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells);
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines, for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 other;
XX
Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 AGGCCAAG 18
Db 10 AGGCCAAG 2
XX
RESULT 56
ABL52193/c
ID ABL52193 standard; DNA; 10 BP.
XX
AC ABL52193;
XX
DT 12-JUL-2002 (first entry)
XX
DE Human PER1 preferred oligonucleotide primer SEQ ID NO:118.
XX
KW Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
KW polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
KW single nucleotide polymorphism; SNP; gene; primer; ss.
XX
OS Homo sapiens.
XX

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PN WO200222650-A2.
XX
XX 21-MAR-2002.
XX
XX 13-SEP-2001; 2001WO-US28780.
XX
XX 13-SEP-2000; 2000US-232468P.
XX
XX (GENA-) GENNAISSANCE PHARM INC.
XX
XX Duda A, Kilem SE, Koshy B;
XX
XX WPI; 2002-393941/42.
XX
XX Novel isolated human period Drosophila homolog 1 polynucleotide, useful
PT for therapeutic purposes, for studying the expression and function of
PT the polynucleotide, and for expressing the homolog -
XX
XX Claim 19; Page 15; 162pp; English.
XX
XX The present invention describes an isolated human period (Drosophila)
CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
CC polymorphic variant for a reference sequence (AB152077) for the PER1 gene
CC or its fragment, or a polymorphic variant of a reference sequence
CC (AB152078) for a PER1 cDNA or its fragment. The present invention also
CC describes methods for genotyping and haplotyping the PER1 gene of an
CC individual. (I) is useful in studying the expression and function of
CC PER1, and in expressing PER1 protein for use in screening for candidate
CC drugs to treat diseases related to PER1 activity. (I) is useful for
CC therapeutic purposes. A recombinant non-human organism transformed or
CC transfected with (I) can be used for studying expression of the PER1
CC isogene in vivo, for in vivo screening and testing of drugs targeted
CC against PER1 protein, and for testing the efficacy of therapeutic agents
CC and compounds for disorders associated with circadian rhythm regulation.
CC The present sequence represents a preferred oligonucleotide primer
CC for human PER1, which is used in the exemplification of the present
CC invention.
CC
SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 other;
Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CGGGCCAGG 12
Db 10 CGGGCCAGG 2
RESULT 57
AAS19877/c
ID AAS19877 standard; DNA; 10 BP.
XX
XX AAS19877;
XX
XX 08-MAY-2002 (first entry)
XX
XX Oligonucleotide #57 to detect human RANGAP1 gene polymorphisms.
DE
XX
XX Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping
KM chromosome 2q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
KM cancer; irregular cell cycle associated disorder; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200179240-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US12455.
XX
XX 17-APR-2000; 2000US-198072P.
XX

PA (GENA-) GENNAISSANCE PHARM INC.
XX
XX Chew A, Choi JY, Koshy B;
XX
XX WPI; 2002-075068/10.
XX
XX Genotyping human Ran GTPase activating protein 1 gene of individual for
PT determining haplotype of individual, involves determining identity of
PT nucleotide pair at specific polymorphic sites for two copies of the
PT gene -
XX
XX Claim 17; Page 16; 148pp; English.
XX
XX The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC genotyping the RANGAP1 gene. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC primer-extension oligonucleotides for detecting the RANGAP1 gene
CC polymorphisms. The polynucleotides and screened compounds are useful for
CC treatment of diseases associated with RANGAP1 activity, such as
CC cancer and other disorders associated with an irregular cell cycle.
CC AAS19821-AAS19898 represent primer-extension oligonucleotides for
CC detecting human RANGAP1 gene polymorphisms.
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;
Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CGGGCCAGG 12
Db 10 CGGGCCAGG 2
RESULT 58
AAD26166
ID AAD26166 standard; DNA; 10 BP.
XX
XX AAD26166;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human endothelin 2 (EDN2) gene polymorphism detecting primer #5.
DE
XX
XX Human; endothelin 2; EDN2; polymorphic site; PS; therapy; hypertension;
KM drug screening; cardiovascular disorder; renal insufficiency; ASO;
KM allele specific oligonucleotide; cerebroprotective; polymorphism;
KM hypotensive; cerebrovascular condition; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200190118-A2.
XX
XX 29-NOV-2001.
XX
XX 21-MAY-2001; 2001WO-US16433.
XX
XX 19-MAY-2000; 2000US-205761P.
XX
XX (GENA-) GENNAISSANCE PHARM INC.
XX
XX Kazeml A, Koshy B, Tanguay DA;
XX
XX WPI; 2002-083075/11.
XX
XX New human endothelin 2 (EDN2) polymorphic variants and encoding genes,
PT useful in expressing EDN2 protein for screening candidate drugs to
PT treat diseases related to EDN2 activity -
XX
XX Claim 18; Page 15; 91pp; English.
XX

CC The invention relates to genetic variants of human endothein 2 (EDN2)
CC gene. EDN2 gene contains 17 polymorphic sites PS1-PS17. The polymorphic
CC variants are useful in studying the expression and function of EDN2,
CC in expressing EDN2 protein for use in screening for candidate drugs to
CC treat diseases related to EDN2 activity, in studying the effect of the
CC variation on the biological activity of EDN2, and the binding affinity
CC of candidate drugs targeting EDN2 for the treatment of hypertension,
CC cardiovascular disorders, renal insufficiency and cerebrovascular
CC conditions. The haplotyping methods are useful in validating EDN2 as
CC a candidate target for treating a specific condition or disease
CC predicted to be associated with EDN2 activity, or in the design of
CC clinical trials of candidate drugs for treating a specific condition
CC or disease associated with EDN2 activity. Allele specific
CC oligonucleotides (ASO) are used as probes and primers, and for
CC detecting polymorphism in EDN2 gene. The present sequence is a
CC primer used to detect polymorphism in human EDN2 gene.

SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCCAGG 12
|||
2 CGGGCCAGG 10

Db

RESULT 59
ABQ81865/c
ID ABQ81865 standard; DNA; 11 BP.

AC ABQ81865;
XX

DT 19-NOV-2002 (first entry)
XX

DE Kaposi's Sarcoma SAGE library Tag No.15 SEQ ID NO:15.
XX

XX Human; Kaposi's sarcoma; tumour; angiogenesis; tag; ss.
XX

OS Homo sapiens.
XX

PN BP125233-A2.
XX

PD 24-JUL-2002.
XX

PF 23-JAN-2002; 2002EP-0075264.
XX

PR 23-JAN-2001; 2001EP-0200228.
XX

PR 28-SEP-2001; 2001EP-0203703.
XX

PR 28-SEP-2001; 2001US-325722P.
XX

XX (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX

XX Van Der Kuyt AC, Cornelissen M;
XX

XX WPI; 2002-668396/72.
XX

PT Determining presence of a tumor cell or angiogenesis, and the
XX effectiveness of treatment, by detecting the presence of marker genes
XX is useful to detect and monitor treatment of Kaposi's Sarcoma
XX

PS Claim 12; Page 8; 38pp; English.
XX

CC The present invention describes a method for determining if an individual
CC has a tumour cell or site of angiogenesis, or if a treatment is effective
CC in changing angiogenesis or changing a status of a set of target cells,
CC comprising determining if a sample of the subject has an expression
CC product of at least one marker gene. Also described is a compound capable
CC of altering the expression or activity of Keratin 14, TIE 1, Sallodhesin
CC or 'Stigle' in a cell. Peripheral blood mononuclear cell (PBMC)-expressed
CC Keratin 14, TIE 1, Sallodhesin or 'Stigle', and kits containing them from
CC the present invention can be used in a diagnostic method, particularly as

CC an indicator of angiogenesis or to determine presence of a tumour cell.
CC The method of the invention is suitable to determine within a few days if
CC a certain treatment against Kaposi's Sarcoma is successful. ABQ81861 to
CC ABQ82006 represent nucleotide sequence used in the exemplification of the
CC present invention.

SQ Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGCC 14
|||
11 GGCCAGGCC 3

Db

RESULT 60
ABV62890/c
ID ABV62890 standard; cDNA; 11 BP.

AC ABV62890;
XX

DT 21-OCT-2002 (first entry)
XX

DE Human skin EST 676.
XX

XX Human; skin; dermatological; vulnery; antiseborrhoeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX

OS Homo sapiens.
XX

PN WO200253774-A2.
XX

PD 11-JUL-2002.
XX

PF 20-DEC-2001; 2001WO-BP15179.
XX

PR 03-JAN-2001; 2001DE-1000127.
XX

XX (HENK) HENKEL KGAA.
XX

PA Petersohn D, Conradt M, Hofmann K;
XX

PI WPI; 2002-590638/63.
XX

DR WPI; 2002-590638/63.
XX

XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer
XX

PT Disclosure; Page 44; 1345pp; German.
XX

PS The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis, to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention.

CC

CC

CC

SQ Sequence 11 BP; 1 A; 2 C; 3 G; 5 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CAGGCCAA 17

Db			10 CAGGCCCAA 2
	RESULT 61		
ID	ABV64419/c		
XX	ABV64419 standard; CDNA; 11 BP.		
AC	ABV64419;		
XX			
DT	21-OCT-2002 (first entry)		
XX			
DE	Human skin EST 2205.		
XX			
KW	Human; skin; dermatological; vulnerrary; antipsoriatic; antiseborrhagic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.		
XX			
OS	Homo sapiens.		
XX	WO200253774-A2.		
FN			
XX	11-JUL-2002.		
PD			
PF	20-DEC-2001; 2001WO-EP15179.		
XX			
FR	03-JAN-2001; 2001DE-1000127.		
XX			
PA	(HENK) HENKEL KGAA.		
XX			
PI	Petersohn D, Conradt M, Hofmann K;		
XX			
DR	WI; 2002-590638/63.		
XX			
PT	In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer -		
PT			
PS	Disclosure; Page 86; 1345pp; German.		
XX			
CC	The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.		
CC	(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; icthyovrosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention.		
XX			
SQ	Sequence 11 BP; 1 A; 2 C; 4 G; 4 T; 0 other;		
OY			
DB	Query Match 45.0%; Score 9; DB 1; Length 11; Best Local Similarity 100.0%; Pred.No. 81; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
DB	8 CCAGGCCCA 16 11 CCAGGCCCA 3		
	RESULT 62		
ID	ABV64637/c		
XX	ABV64637 standard; CDNA; 11 BP.		
AC	ABV64637;		
XX			
DT	21-OCT-2002 (first entry)		
XX			
DE	Human skin EST 2423.		

XX		Human; skin; dermatological; vulnery; antipsoriatic; antiacne; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW		immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KX		psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX		
OS	Homo sapiens.	
XX		
PN	WO200253774-A2.	
PD	11-JUL-2002.	
XX		
PF	20-DEC-2001; 2001WO-EPI5179.	
XX		
PR	03-JAN-2001; 2001DE-1000127.	
XX		
PA	(HENK) HENKE KGAA.	
PI	Petersohn D, Conradt M, Hofmann K;	
XX		
DR	WPI; 2002-590638/63.	
XX		
PT	In vitro identification of skin-expressed genes, useful for determining	
PT	homeostasis and identifying cosmetic or pharmaceutical agents against	
PT	e.g. skin cancer -	
XX		
PS	Disclosure; Page 92; 1345pp; German.	
CC	The invention relates to in vitro identification (M1) of genes expressed	
CC	in the skin of humans or animals by subjecting a mixture of genetically	
CC	encoded factors from skin, to serial analysis of gene expression (SAGE)	
CC	so as to identify skin-expressed genes and quantify their expression.	
CC	(M1) is useful for identifying genes involved in skin homeostasis; to	
CC	determine skin homeostasis and to test agent (A) that maintains or	
CC	promotes skin homeostasis or that can be used for treating skin	
CC	disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;	
CC	ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;	
CC	rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the	
CC	skin. The present sequence is that of a human expressed sequence tag	
CC	(EST) of the invention.	
XX		
SQ	Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;	
	Query Match	45.0%; Score 9; DB 1; Length 11;
	Best Local Similarity	100.0%; Pred. No. 81;
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	6 GGCCAGGCC 14 	
DB	11 GGCCAGGCC 3	
	RESULT 63	
	ABV68400/C	
ID	ABV68400 standard; cDNA; 11 BP.	
AC	ABV68400;	
XX		
DT	21-OCT-2002 (first entry)	
XX		
DE	Human skin EST 6186.	
XX		
KW	Human; skin; dermatological; vulnerary; antipsoriatic; antiacne; antiinflammatory; cytostatic; SAGE; neurodermatitis;	
KV	immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;	
KW	psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200253774-A2.	
PD	11-JUL-2002.	
XX		
PF	20-DEC-2001; 2001WO-EPI5179.	
XX		

```
PR 03-JAN-2001; 2001DE-1000127.
XX
XX (HENK ) HENKEL KGAA.
PA
XX Petersohn D, Conradt M, Hofmann K;
PI
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
XX Disclosure; Page 197; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
XX Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 other;
SQ
Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 CCAGGCCAA 16
Db 11 CCAGGCCAA 3
RESULT 64
ABV68594/c
ID ABV68594 standard; cDNA; 11 BP.
XX
XX ABV68594;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Human skin EST 6380.
DE
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200253774-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 20-DEC-2001; 2001WO-EP15179.
PF
XX
XX 03-JAN-2001; 2001DE-1000127.
PR
XX
XX (HENK ) HENKEL KGAA.
PA
XX Petersohn D, Conradt M, Hofmann K;
PI
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
XX Disclosure; Page 202; 1345pp; German.
```

```
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
XX Sequence 11 BP; 0 A; 2 C; 5 G; 4 T; 0 other;
SQ
Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 CCAGGCCAA 16
Db 10 CCAGGCCAA 2
RESULT 65
ABV70311/c
ID ABV70311 standard; cDNA; 11 BP.
XX
XX ABV70311;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Human skin EST 8097.
DE
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200253774-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 20-DEC-2001; 2001WO-EP15179.
PF
XX
XX 03-JAN-2001; 2001DE-1000127.
PR
XX
XX (HENK ) HENKEL KGAA.
PA
XX Petersohn D, Conradt M, Hofmann K;
PI
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
XX Claim 24; Page 258; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
```

```

XX SQ Sequence 11 BP; 1 A; 2 C; 3 G; 5 T; 0 other;
Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CAGGCCCAA 17
Db 10 CAGGCCCAA 2

RESULT 66
ABV71840/C
ID ABV71840 standard; cDNA; 11 BP.
XX
XX ABV71840;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Human skin EST 9626.
DE
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200253774-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 20-DEC-2001; 2001WO-EP15179.
PF
XX
XX 03-JAN-2001; 2001DE-1000127.
PR
XX
XX (HENK ) HENKEL KGAA.
PA
XX
XX Petersohn D, Conradt M, Hofmann K;
PI
XX
XX WPI; 2002-590638/63.
DR
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
XX Claim 24; Page 311; 1345pp; German.
PS
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
XX Sequence 11 BP; 1 A; 2 C; 4 G; 4 T; 0 other;
SQ
Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CAGGCCCAA 16
Db 11 CAGGCCCAA 3

RESULT 67

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```

AAS19798/C
ID AAS19798 standard; DNA; 15 BP.
XX
XX AAS19798;
AC
XX
XX 08-MAY-2002 (first entry)
DT
XX
XX ASO primer #56 to detect human RANGAP1 gene polymorphisms.
DE
XX
XX Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping
KW chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
KW cancer; irregular cell cycle associated disorder; ASO; primer; ss;
KW allele-specific oligonucleotide.
XX
XX Homo sapiens.
OS
XX
XX WO200179240-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 17-APR-2001; 2001WO-US12455.
PF
XX
XX 17-APR-2000; 2000US-198072P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Chew A, Choi JY, Koshy B;
PI
XX
XX WPI; 2002-075068/10.
DR
XX
XX Genotyping human Ran GTPase activating protein 1 gene of individual for
PT determining haplotype of individual, involves determining identity of
PT nucleotide pair at specific polymorphic sites for two copies of the
PT gene -
XX
XX Claim 15; Page 15; 148pp; English.
PS
XX
XX The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC genotyping the RANGAP1 gene. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC primer-extension oligonucleotides for detecting the RANGAP1 gene
CC polymorphisms. The polymorphisms and screened compounds are useful for
CC treatment of diseases associated with RANGAP1 activity, such as
CC cancer and other disorders associated with an irregular cell cycle.
CC AAS19743-AAS19820 represent ASO primers for detecting human RANGAP1
CC gene polymorphisms.
XX
XX Sequence 15 BP; 3 A; 6 C; 5 G; 0 U; 1 other;
SQ
Query Match 44.0%; Score 8.8; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCCGGCCACG 12
Db 12 GTCTGCGCCCG 1

RESULT 68
AAV60744/C
ID AAV60744 standard; DNA; 18 BP.
XX
XX AAV60744;
AC
XX
XX 08-DEC-1998 (first entry)
DT
XX
XX Primer #2 for human CDK4 codons 1-163.
DE
XX
XX PCR primer; amplification; yeast; UAS; upstream activating sequence;
KW transcription terminator; cell cycle; Upstream Activation Sequence; UAS;
KW promoter; phosphorylation; cyclin; cyclin-dependent kinase; CDK; vector;

```

KM cyclin kinase inhibitor; CKI; growth; wound healing; cancer therapy; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX W09816660-A1.
 PN W09816660-A1.
 XX 23-APR-1998.
 PD 23-APR-1998.
 XX 16-OCT-1997; 97WO-US18608.
 PF 16-OCT-1997; 97WO-US18608.
 XX 27-NOV-1996; 96US-0031968.
 PR 16-OCT-1996; 96US-0029127.
 XX (BITT-) BITTECH INC.
 PA (BITT-) BITTECH INC.
 PI Bitter GA;
 XX Bitter GA;
 DR WPI; 1998-251302/22.
 XX
 PT Screening for agents that effect cell cycle regulatory proteins -
 PT using a cell line that expresses a reporter gene in response to
 PT regulation through phosphorylation by a cyclin/CDK system
 XX
 PS Example 4; Page 75; 93pp; English.
 XX
 CC Primers AAV60743-V60745 were used to PCR amplify codons 1-163 of the
 CC human cyclin-dependent kinase 4 (hcdk4). The amplified product was used
 CC to generate a fusion protein comprising part of the hcdk4 sequence
 CC linked to codons 154-302 of the yeast PHO5 gene. The fusion protein is
 CC used to screen for compounds that affect mammalian cell cycle regulatory
 CC proteins. The method comprises administering a compound to a cell line,
 CC which contains a reporter gene linked to an Upstream Activation Sequence
 CC (UAS) and a promoter, where the UAS binds a transcription control factor
 CC (TCF) which is regulated through cyclin/cyclin-dependent kinase (CDK)
 CC phosphorylation. Also included in the construct is an effector gene
 CC providing a gene product to permit normal cyclin/CDK regulation of the
 CC TCF. Expression of the reporter gene is then analysed in the cell line,
 CC thereby determining whether the compound affects the normal regulation.
 CC The method can be used to identify inhibitors and activators of
 CC mammalian cell cycle regulatory proteins, especially inhibitors and
 CC activators of cyclins, CDKs, cyclin/CDK complexes, cyclin kinase
 CC inhibitors (CKIs), and cyclin/CDK/CKI complexes. The identified agents
 CC can be used for stimulating growth of cells (as in wound healing), or
 CC regulating excessive cell growth and division (as in cancer therapy).
 CC
 SQ Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 other;
 Query Match 44.0%; Score 8.8; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 6 GGGCAGGCCCAA 17
 DB 12 GGGCTGGCCAGA 1
 RESULT 69
 AAQ96791
 ID AAQ96791 standard; DNA; 10 BP.
 XX AAQ96791;
 AC AAQ96791;
 XX 26-MAR-1996 (first entry)
 DT 26-MAR-1996 (first entry)
 XX HIV-1 N14-3 nef gene nucleotide deletion 386.
 DE HIV-1 N14-3 nef gene nucleotide deletion 386.
 XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
 KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
 OS Human immunodeficiency virus type 1.
 XX Human immunodeficiency virus type 1.
 PN W09521912-A1.
 XX W09521912-A1.

PD 17-AUG-1995.
 XX 17-AUG-1995.
 XX 14-FEB-1995; 95WO-AU00063.
 PF 14-FEB-1995; 95WO-AU00063.
 XX 23-DEC-1994; 94AU-0000284.
 PR 14-FEB-1994; 94AU-0003864.
 PR 21-FEB-1994; 94AU-0004002.
 XX (AURE-) AUSTRALIAN RED CROSS SOC NSW DIV.
 PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
 PI Cooper D, Crowe S, Deacon NJ, Learmont JC, McPhee DA;
 XX Cooper D, Crowe S, Deacon NJ, Learmont JC, McPhee DA;
 DR WPI; 1995-293115/38.
 XX WPI; 1995-293115/38.
 PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene
 PT or LTR region - can be used in a vaccine to inhibit/reduce
 PT productive infection in an individual by a pathogenic strain
 XX
 PS Claim 13; Page 193; 301pp; English.
 XX
 CC Attenuation of pathogenic HIV-1 strain N14-3 involves deletion of 1
 CC or more deca-nucleotides (AAQ96406-Q97018) from the nef gene and/or
 CC 1 or more deca-nucleotides (AAQ97019-Q97166) from the LTR region; the
 CC sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene
 CC (AAQ96141). The resulting avirulent HIV strains are still capable of
 CC inducing an immune response in humans, and enable the generation of
 CC therapeutic, diagnostic and targeting agents against HIV-1 infection.
 CC
 SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 U; 0 other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 3 CCGGGCCAGG 12
 DB 1 CAGGGCCAGG 10
 RESULT 70
 AAT29327/C
 ID AAT29327 standard; DNA; 10 BP.
 XX AAT29327;
 AC AAT29327;
 XX 25-MAR-2003 (updated)
 DT 25-MAR-2003 (updated)
 XX 28-JUN-1996 (first entry)
 DE 28-JUN-1996 (first entry)
 XX 5'-primer for mammalian G-protein coupled receptor coding sequences.
 DE 5'-primer for mammalian G-protein coupled receptor coding sequences.
 XX 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
 KW characterisation; biological samples; PCR amplification; indexing;
 KW identification; cloning; analysis; genes; genome mapping;
 KW disease diagnosis; ss.
 XX
 OS Synthetic.
 XX
 PN W09531574-A1.
 XX W09531574-A1.
 PD 23-NOV-1995.
 XX 12-MAY-1995; 95WO-US06032.
 PF 12-MAY-1995; 95WO-US06032.
 XX 16-MAY-1994; 94US-0242887.
 PR 16-MAY-1994; 94US-0242887.
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX Lopeznielo CE, Nigam SK;
 PI Lopeznielo CE, Nigam SK;
 XX WPI; 1996-010958/01.
 DR WPI; 1996-010958/01.
 XX
 PT Characterisation of nucleotide sequences using primer pairs - by PCR

PT amplification and indexing of amplification prods. w.r.t. primers
 PT used for genome mapping and disease diagnosis
 XX
 PS Claim 46; Page 55; 72pp; English.
 CC The 5'-primers AAT9262-382, and the complementary 3'-primers derived
 CC from them, which target mammalian G-protein coupled receptor coding
 CC sequences, together comprise a PCR primer kit. The kit is used in a
 CC new method for the characterisation of nucleic acid sequences obd.
 CC from mammalian biological samples, which comprises PCR amplification
 CC and indexing of the prods. w.r.t the primer pair that hybridised to
 CC its delineating subsequences. The method may be used in the
 CC identification, cloning and analysis of genes, e.g. in genome
 CC mapping, and disease diagnosis.
 CC (updated on 25-MAR-2003 to correct PI field.)
 CC
 XX Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;.
 SQ
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 4 CGGCGCCAGGC 13
 Db 10 CAGGCCAGGC 1
 RESULT 71
 AAV50125/c
 ID AAV50125 standard; DNA; 10 BP.
 XX
 AC AAV50125;
 XX
 DT 21-OCT-1998 (first entry)
 XX
 DE Yeast tag for NORF gene locus NORF15.
 XX
 KM Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle;
 KM regulation; eukaryotic cell; antifungal; SAGE tag; gene expression;
 KM berial analysis of gene expression; probe; ss.
 XX
 OS Saccharomyces cerevisiae.
 OS Synthetic.
 OS
 XX WO9832847-A2.
 PN 30-JUL-1998.
 XX
 PD 22-JAN-1998; 98WO-US01216.
 XX
 PF 23-JAN-1997; 97US-0035917.
 XX
 PR (UYUO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PA Kinzler KM, Velculescu VE, Vogelstein B;
 PI
 XX WPI; 1998-427943/36.
 DR
 XX Yeast transcriptome - useful for modulating eukaryotic cell, for
 PT screening antifungal agents, and for identifying genes in cell cycle
 PT progression
 PT
 XX Claim 1; Page 23; 44pp; English.
 PS
 XX Yeast transcriptome is encoded by a DNA molecule comprising a yeast
 CC gene involved in cell cycle progression selected from the group of
 CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
 CC tags for highly expressed genes and NORF genes are given in AAV50051 to
 CC AAV50345. The present invention describes: (1) a method of using yeast
 CC genes to modulate the cell cycle which comprises administering to a cell
 CC an isolated DNA molecule comprising a yeast gene which is involved in
 CC cell cycle progression selected from differentially expressed genes
 CC (SAGE tags given in AAV50051 to AAV50345); (2) a method for screening

CC candidate antifungal drugs which comprises contacting a test substance
 CC with a yeast cell and monitoring expression of a yeast gene which is
 CC involved in cell cycle progression; (3) a method of identifying human
 CC genes which are involved in cell cycle progression which comprises
 CC hybridizing a probe comprising at least 10 contiguous nucleotides of a
 CC yeast gene which is differentially expressed between at least 2 phases
 CC selected from the log phase, the S phase and the G2/M phase; and (4) a
 CC probe for ascertaining the phase in the cell cycle, where the probe
 CC comprises at least 14 contiguous nucleotides of a NORF gene (SAGE tags
 CC given in AAV50051 to AAV50345), or as an array of probes on a solid
 CC support.
 CC
 XX Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;
 SQ
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 6 GGCCAGGCCA 15
 Db 10 GGCCAGGCCA 1
 RESULT 72
 AAX54917
 ID AAX54917 standard; DNA; 10 BP.
 XX
 AC AAX54917;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE C/EBP-beta antisense oligonucleotide fragment.
 XX
 KM Antisense oligonucleotide; multiple target; antisense treatment;
 KM impaired respiration; inflammation; lung disease;
 KM pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KM acute asthma; allergy; asthma; impeded respiration;
 KM respiratory distress syndrome; pain; cystic fibrosis;
 KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KM prostate cancer; ss.
 XX
 OS Synthetic.
 OS
 XX WO9913886-A1.
 PN 25-MAR-1999.
 XX
 PD 17-SEP-1998; 98WO-US19419.
 XX
 PF 09-JUN-1998; 98US-0093972.
 XX
 PR 17-SEP-1997; 97US-0059160.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PI
 XX Nyce JW;
 PI
 XX WPI; 1999-229400/19.
 DR
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 PT
 XX Disclosure; Page 68; 120pp; English.
 PS
 XX The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides

CC may be derived from sequences AAX55272-74. These multiple target
 CC oligonucleotides (specifically AAX55180-271) can be used for the
 CC antisense treatment of diseases and conditions. Typical diseases and
 CC conditions are those associated with impaired respiration and
 CC inflammation, including lung diseases, pulmonary vasoconstriction,
 CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
 CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
 CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
 CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
 CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
 CC hepatic metastases, as well as all types of cancers which may metastasize
 CC or have metastasized to the lungs, including breast and prostate cancer.
 CC
 XX Sequence 10 BP; 0 A; 4 C; 6 G; 0 U; 0 other;
 SQ
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 CGGGCCAGGC 13
 |||||
 Db 1 CGGGCCCGGC 10
 RESULT 73
 ID AAF20486 standard; DNA; 10 BP.
 XX AAF20486;
 DT 14-MAR-2001 (first entry)
 DE Human C/EBP polynucleotide fragment #2053.
 XX
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200062736-A2.
 PN
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 PI
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 XX Claim 14; Page 262; 1592pp; English.
 XX
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,

CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 CC
 XX Sequence 10 BP; 0 A; 4 C; 6 G; 0 U; 0 other;
 SQ
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 CGGGCCAGGC 13
 |||||
 Db 1 CGGGCCCGGC 10
 RESULT 74
 ID AAC73935 standard; cDNA; 10 BP.
 XX AAC73935/c
 XX AAC73935;
 AC
 XX 02-FEB-2001 (first entry)
 DT
 XX Human dendritic cell cDNA base sequence oligonucleotide #22.
 DE
 XX Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 KW human; autoimmune disease; tumour; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200060074-A1.
 PN
 XX 12-OCT-2000.
 PD
 XX 30-MAR-2000; 2000WO-JP02019.
 PF
 XX 01-APR-1999; 99JP-0095481.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA Hashimoto S, Matsushima K, Suzuki T;
 XX
 XX WPI; 2000-619172/59.
 DR
 XX Groups of genes expressed in human dendritic cells at a greater or
 PT lesser extent than in monocytes for investigation and diagnosis of
 PT autoimmune disease and tumors -
 XX
 XX Claim 1; Page 9; 95pp; Japanese.
 PS
 XX The present invention describes a group of genes consisting of 100 genes

CC which are highly expressed in human dendritic cells; a group of genes
CC which are expressed at a higher frequency in human dendritic cells than
CC in human monocytes; and a group of genes which are expressed at lower
CC frequency in human dendritic cells than in human monocytes. Each group
CC of genes are characterised in that cDNAs of these genes respectively
CC have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013),
CC SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300
CC (AAC74114 to AAC74213), each is continuous with the base sequence
CC 5'-CATG-3', located most closely to the poly-A region. The sequences can
CC be used for the investigation of the role and mechanism of the
CC involvement of dendritic cells in the immune system and for the study and
CC diagnosis of diseases in which dendritic cells play a significant role,
CC e.g. cancers and autoimmune diseases.

XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCGAGGCCA 16
DB 10 GCCTGGCCAA 1

RESULT 75

ID AAC74189/c
AAC74189 standard; cDNA; 10. BP.

XX AAC74189;

DT 02-FEB-2001 (first entry)

XX Human monocyte and dendritic cell expressed gene oligonucleotide #276.

XX Human, dendritic cell; monocyte; immune system; diagnosis; cancer;

KW autoimmune disease; tumour; ss.

XX Homo sapiens.

PN WO200060074-A1.

PD 12-OCT-2000.

PF 30-MAR-2000; 2000WO-JP02019.

PR 01-APR-1999; 99JP-0095481.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PI Hashimoto S, Matsushima K, Suzuki T;

DR WPI; 2000-619172/59.

XX Groups of genes expressed in human dendritic cells at a greater or
PT lesser extent than in monocytes for investigation and diagnosis of
PT autoimmune disease and tumors -

PS Claim 19; Page 16; 95bp; Japanese.

XX The present invention describes a group of genes consisting of 100 genes
CC which are highly expressed in human dendritic cells; a group of genes
CC which are expressed at a higher frequency in human dendritic cells than
CC in human monocytes; and a group of genes which are expressed at lower
CC frequency in human dendritic cells than in human monocytes. Each group
CC of genes are characterised in that cDNAs of these genes respectively
CC have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013),
CC SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300
CC (AAC74114 to AAC74213), each is continuous with the base sequence
CC 5'-CATG-3', located most closely to the poly-A region. The sequences can
CC be used for the investigation of the role and mechanism of the
CC involvement of dendritic cells in the immune system and for the study and
CC diagnosis of diseases in which dendritic cells play a significant role,

CC e.g. cancers and autoimmune diseases.

XX
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GGGCCAGGCC 14
DB 10 GTGCCAGGCC 1

RESULT 76

ID AAA34364
AAA34364 standard; DNA; 10 BP.

XX AAA34364;

DT 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide SEQ ID NO:2053.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;

KW phosphorothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

KW antiallergic; antiaschmatic; cyostatic; analgesic; impaired airway;

KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

PN WO200009525-A2.

PD 24-FEB-2000.

PF 03-AUG-1999; 99WO-US17712.

PR 03-AUG-1998; 98US-0095212.

XX (UYEC-) UNIV EAST CAROLINA.

PI Nyce JW;

DR WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary

PT vasoconstriction, inflammation, allergies, asthma, hypertension,

PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers -

XX Disclosure; Page 523; 1343pp; English.

XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antisthmatic, cyostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present

CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA23232 to AAA3392) are specifically claimed ONS from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.

XX
 XX Sequence 10 BP; 0 A; 4 C; 6 G; 0 U; 0 other;

SO Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGGCGCCAGGC 13
 |||||
 1 CGGCGCCGGC 10

Db

RESULT 77
 AAZ77977/c
 ID AAZ77977 standard; DNA: 10 BP.
 XX
 XX AAZ77977;
 AC
 XX 10-APR-2000 (first entry)
 DT
 XX Human dendritic cell SAGE tag, SEQ ID NO:405.
 DE
 XX
 KM SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KM APC; monocyte-derived dendritic cell; differential gene expression;
 KM immunostimulatory cofactor; costimulatory factor; CTL;
 KM cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO965924-A2.
 PD
 XX 23-DEC-1999.
 PF 18-JUN-1999; 99NO-US13800.
 XX
 XX 19-JUN-1998; 98US-0089833.
 PR 19-JUN-1998; 98US-0089844.
 PR 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089878.
 PR 19-JUN-1998; 98US-0089991.
 PR 19-JUN-1998; 98US-0089992.
 PR 19-JUN-1998; 98US-0089993.
 PR 19-JUN-1998; 98US-0089994.
 PR 19-JUN-1998; 98US-0089997.
 PR 19-JUN-1998; 98US-0089999.
 PR 19-JUN-1998; 98US-0090000.
 PR 19-JUN-1998; 98US-0090035.
 PR 19-JUN-1998; 98US-0090036.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 PR 19-JUN-1998; 98US-0090042.
 PR 19-JUN-1998; 98US-0090043.
 PR 19-JUN-1998; 98US-0090044.
 PR 19-JUN-1998; 98US-0090045.
 PR 19-JUN-1998; 98US-0090047.
 PR 19-JUN-1998; 98US-0090048.
 PR 19-JUN-1998; 98US-0090072.
 PR 19-JUN-1998; 98US-0090076.
 PR 19-JUN-1998; 98US-0090077.
 PR 19-JUN-1998; 98US-0090078.
 PR 19-JUN-1998; 98US-0090079.
 PR 19-JUN-1998; 98US-0090080.
 PR 08-DEC-1998; 98US-0111715.
 XX
 XX (GENZ) GENZYME CORP.
 PA

PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 XX Roberts BL, Shankara S;
 PI
 XX WPI, 2000-106077/09.
 DR
 XX
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer -
 XX
 PS Claim 1; Page 76; 130pp; English.

XX
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or
 CC ESTs (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can
 CC lyse the tumour cells. Immunostimulatory cofactors also being required
 CC for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen, to modulate the genotype of an APC, to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC, and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell
 CC differentially expressed genes, or of their encoded proteins, can be used
 CC to identify cells as belonging to the monocyte lineage. Cells containing
 CC these genes can be used in active immunotherapy (or to stimulate
 CC production of a population of antigen-specific effector cells) and
 CC vectors containing them are used in gene therapy. Co-administration of
 CC tumour antigens and APC-associated costimulatory factors ensures adequate
 CC antigen presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells.
 CC
 XX
 SO Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;

QY 7 GCCAGGCCAA 16
 |||||
 10 GCCAGGCCCA 1

Db

RESULT 78
 AAZ78898
 ID AAZ78898 standard; DNA: 10 BP.
 XX
 XX AAZ78898;
 AC
 XX 10-APR-2000 (first entry)
 DT
 XX Human dendritic cell SAGE tag, SEQ ID NO:1326.
 DE
 XX
 KM SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KM APC; monocyte-derived dendritic cell; differential gene expression;
 KM immunostimulatory cofactor; costimulatory factor; CTL;
 KM cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX

PN WO965924-A2.
 XX 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US13800.
 XX 19-JUN-1998; 98US-0089833.
 PR 19-JUN-1998; 98US-0089844.
 PR 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089878.
 PR 19-JUN-1998; 98US-0089991.
 PR 19-JUN-1998; 98US-0089992.
 PR 19-JUN-1998; 98US-0089993.
 PR 19-JUN-1998; 98US-0089994.
 PR 19-JUN-1998; 98US-0089997.
 PR 19-JUN-1998; 98US-0089999.
 PR 19-JUN-1998; 98US-0090000.
 PR 19-JUN-1998; 98US-0090035.
 PR 19-JUN-1998; 98US-0090036.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 PR 19-JUN-1998; 98US-0090042.
 PR 19-JUN-1998; 98US-0090043.
 PR 19-JUN-1998; 98US-0090044.
 PR 19-JUN-1998; 98US-0090045.
 PR 19-JUN-1998; 98US-0090047.
 PR 19-JUN-1998; 98US-0090048.
 PR 19-JUN-1998; 98US-0090072.
 PR 19-JUN-1998; 98US-0090076.
 PR 19-JUN-1998; 98US-0090077.
 PR 19-JUN-1998; 98US-0090078.
 PR 19-JUN-1998; 98US-0090079.
 PR 19-JUN-1998; 98US-0090080.
 PR 08-DEC-1998; 98US-0111715.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106077/09.
 XX
 PT Isolated polynucleotides differentially expressed in antigen-presenting
 XX cells, useful in gene vaccines against cancer -
 PS
 XX Claim 1; Page 103; 130pp; English.

CC these genes can be used in active immunotherapy (or to stimulate
 CC production of a population of antigen-specific effector cells) and
 CC vectors containing them are used in gene therapy. Co-administration of
 CC tumour antigens and APC-associated costimulatory factors ensures adequate
 CC antigen presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells.
 XX
 SQ Sequence 10 BP, 5 A; 2 C; 2 G; 1 T; 0 other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 AGCCCAAGT 19
 Db 1 AGACCAAGT 10
 RESULT 79
 AA281571
 ID AA281571 standard; DNA; 10 BP.
 XX
 AC AA281571;
 XX
 DT 07-APR-2000 (first entry)
 XX
 XX Metastatic breast tumour cell upregulated transcript tag #805.
 DE
 XX Human: metastatic breast tumour tissue; breast cancer; tag; primer;
 KM non-metastatic breast tumour tissue; gene therapy; anticancer;
 KM antimetastatic; vaccine; diagnosis; ss.
 OS
 XX Homo sapiens.
 XX
 PN WO965928-A2.
 PD 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US13647.
 PF
 XX 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089897.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106079/09.
 XX
 PT Isolated polynucleotides differentially expressed between metastatic
 XX and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 PS
 XX Claim 1; Page 79; 219pp; English.

CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides or as
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.

XX Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 87;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AGGCCAAGT 19

Db 1 AGACCAAGT 10

RESULT 80

AA282444/c

ID AA282444 standard; DNA; 10 BP.

AC AA282444;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #1678.

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KM non-metastatic breast tumour tissue; gene therapy; anticancer;

KX anti-metastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US13647.

PR 19-JUN-1998; 98US-0089853.

PR 19-JUN-1998; 98US-0089997.

PR 19-JUN-1998; 98US-0090039.

PR 19-JUN-1998; 98US-0090040.

PR 19-JUN-1998; 98US-0090041.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

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PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides or as
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.

XX Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 87;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCCAGGCCA 15

Db 10 GGCCAGGCCA 1

RESULT 81

AA282611/c

ID AA282611 standard; DNA; 10 BP.

AC AA282611;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #1845.

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KM non-metastatic breast tumour tissue; gene therapy; anticancer;

KX anti-metastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US13647.

PR 19-JUN-1998; 98US-0089853.

PR 19-JUN-1998; 98US-0089997.

PR 19-JUN-1998; 98US-0090039.

PR 19-JUN-1998; 98US-0090040.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

PI Roberts BL, Shankara S;

CC monitoring and treatment of breast cancer, particularly where metastatic.
CC diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines, for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.

SQ Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 8 CCAGGCCAAA 17
Db 10 CCAGGACAAA 1

RESULT 82
AAZ82634
ID AAZ82634 standard; DNA; 10 BP.
XX AAZ82634;
AC AAZ82634;
XX 07-APR-2000 (first entry)
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1868.
XX
XX Human: metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KM antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
XX MO9965928-A2.
PN 23-DEC-1999.
PD 18-JUN-1999; 99WO-US13647.
PF 19-JUN-1998; 98US-0089853.
XX 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0090039.
XX 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B. L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
XX prevention and treatment of cancer -
XX
XX Claim 1; Page 109; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic

CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines, for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.

SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 11 GGCCAAAGTC 20
Db 1 GGCCAAAGGC 10

RESULT 83
AAZ82905/c
ID AAZ82905 standard; DNA; 10 BP.
XX AAZ82905;
AC AAZ82905;
XX 07-APR-2000 (first entry)
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2139.
XX
XX Human: metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KM antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
XX MO9965928-A2.
PN 23-DEC-1999.
PD 18-JUN-1999; 99WO-US13647.
PF 19-JUN-1998; 98US-0089853.
XX 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0090039.
XX 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B. L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
XX prevention and treatment of cancer -
XX
XX Claim 1; Page 117; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).

CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic
CC diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines, for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.

SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GGGCCAGGCC 14
10 GGGCCAGTCC 1

Db

RESULT 84
AA283555/c
ID AA283555 standard; DNA; 10 BP.

AC AA283555;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #2789.

KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KM antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US13647.

PR 19-JUN-1998; 98US-0089853.

PR 19-JUN-1998; 98US-0089897.

PR 19-JUN-1998; 98US-0090039.

PR 19-JUN-1998; 98US-0090040.

PR 19-JUN-1998; 98US-0090041.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

PI 2000-106079/09.

PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
PS Claim 1; Page 133; 219pp; English.

PS AA280767 to AA283941 represent tags corresponding to distinct

CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic
CC diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines, for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.

SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 CCGGCCAGC 12
10 CAGGCCAGC 1

Db

RESULT 85
AA284116
ID AA284116 standard; DNA; 10 BP.

AC AA284116;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell downregulated transcript tag #3350.

KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KM antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US13647.

PR 19-JUN-1998; 98US-0089853.

PR 19-JUN-1998; 98US-0089897.

PR 19-JUN-1998; 98US-0090039.

PR 19-JUN-1998; 98US-0090040.

PR 19-JUN-1998; 98US-0090041.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

PI 2000-106079/09.

PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
PS Claim 1; Page 148; 219pp; English.

XX AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 U; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GGGCCAGGCC 14
Db 1 GGGCCAGGCC 10
RESULT 86
AA284369/c
ID AA284369 standard; DNA; 10 BP.
XX
AC AA284369;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3603.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX
XX antimetastatic; vaccine; diagnosis; ss.
OS Homo sapiens.
XX
XX
PN WO965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
XX (GENZ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -

XX
PS Claim 1; Page 155; 219pp; English.
XX
XX AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GGGCCAGGCC 14
Db 10 GGGCCAGGCC 1
RESULT 87
AA284683
ID AA284683 standard; DNA; 10 BP.
XX
AC AA284683;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3917.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX
XX antimetastatic; vaccine; diagnosis; ss.
OS Homo sapiens.
XX
XX
PN WO965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
XX
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
XX (GENZ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic

PT and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 XX
 PS Claim 1; Page 163; 219pp; English.
 XX
 CC AA280767 to AA283941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis,
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC Diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 CC
 XX Sequence 10 BP; 1 A; 5 C; 4 G; 0 U; 0 other;
 SO
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GGGCCAGGCC 14
 Db 1 GCCCAGGCC 10
 XX
 RESULT 88
 AA284966/c
 ID AA284966 standard; DNA; 10 BP.
 XX
 AC AA284966;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #4200.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO965928-A2.
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US13647.
 XX
 PR 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089997.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106079/09.

XX
 PT isolated polynucleotides differentially expressed between metastatic
 PT and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 XX
 PS Claim 1; Page 171; 219pp; English.
 XX
 CC AA280767 to AA283941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis,
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC Diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 CC
 XX Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;
 SO
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 GCCAGGCCAA 16
 Db 10 GCCAGGCCCA 1
 XX
 RESULT 89
 AA285815/c
 ID AA285815 standard; DNA; 10 BP.
 XX
 AC AA285815;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #5049.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO965928-A2.
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US13647.
 XX
 PR 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089997.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;

XX WPI; 2000-106079/09.
 DR Isolated polynucleotides differentially expressed between metastatic
 XX and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 PT Claim 1; Page 193; 219pp; English.
 XX
 CC AA280767 to AA283941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis,
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC Diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines, for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;
 XX
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 GCCAGGCCCA 16
 Db 10 GCCCGGCCCA 1
 RESULT 90
 AA285951
 ID AA285951 standard; DNA; 10 BP.
 XX
 AC AA285951;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #5185.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KM non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US13647.
 XX
 PR 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089997.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.

XX Roberts B L, Shankara S;
 XX WPI; 2000-106079/09.
 DR Isolated polynucleotides differentially expressed between metastatic
 XX and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 PT Claim 1; Page 196; 219pp; English.
 XX
 CC AA280767 to AA283941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis,
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC Diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines, for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 XX
 SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 U; 0 other;
 XX
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GGCGCAGCCC 14
 Db 1 GGCGCAGCCC 10
 RESULT 91
 AA286053/C
 ID AA286053 standard; DNA; 10 BP.
 XX
 AC AA286053;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #5287.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KM non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US13647.
 XX
 PR 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089997.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.

PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106079/09.
 XX
 PT Isolated polynucleotides differentially expressed between metastatic
 PT and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 XX
 PS Claim 1; Page 199; 219pp; English.
 XX
 CC AA280767 to AA283941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis,
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC Diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;
 XX
 QY Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Db 4 CCGGCCCAAGC 13
 10 CAGGCCAAGC 1
 XX
 RESULT 92
 AA167394/C
 ID AA167394 standard; DNA; 10 BP.
 XX
 AC AA167394;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE Human FKBP8 gene polymorphism detecting primer.
 XX
 KM FK506-binding protein 8; FKBP8; haplotyping; polymorphism; cancer;
 KM immunosuppression; human; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200172965-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 26-MAR-2001; 2001WO-US09718.
 XX
 PR 24-MAR-2000; 2000US-192125P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 PA Anastasio AE, Bentivegna SC, Choi JY, Klien SE, Koshy B;
 PI Stephens JC;

XX
 DR WPI; 2001-626261/72.
 XX
 PT New haplotypes of the FK506-binding protein 8 gene, useful for
 PT genotyping that gene in individual and to design new therapy for
 PT associated disease such as immunosuppression and cancer -
 XX
 PS Claim 16; Page 15; 98pp; English.
 XX
 CC The invention relates to haplotyping the FK506-binding protein 8 (38KD)
 CC (FKBP8) gene in an individual. The method involves determining the
 CC identity of the nucleotide pair at one or more polymorphic sites selected
 CC from PI to P26 (described in the specification). The invention is useful
 CC to improve the efficiency and reliability of several steps in the
 CC discovery and development of drugs for treating diseases associated with
 CC FKBP8 activity, for example immunosuppression and cancer. Sequences
 CC AA167352-403 represent oligonucleotide primers for detecting FKBP8 gene
 CC polymorphisms by primer extension techniques.
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 other;
 XX
 QY Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Db 8 CCGGCCCAAA 17
 10 CCGGCCCA 1
 XX
 RESULT 93
 ABA06204/C
 ID ABA06204 standard; cDNA; 10 BP.
 XX
 AC ABA06204;
 XX
 DT 10-JAN-2002 (first entry)
 XX
 DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 181.
 XX
 KM Human; hepatocyte; gene expression; hepatopathy; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2001211883-A.
 XX
 PD 07-AUG-2001.
 XX
 PF 31-JAN-2000; 2000JP-0023170.
 XX
 PR 31-JAN-2000; 2000JP-0023170.
 XX
 PA (KAGU-) KAGAKU GIUTTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2001-629566/73.
 XX
 PT Human normal hepatocyte expression gene group -
 PT
 PS Claim 1; Page 9; 26pp; Japanese.
 XX
 CC The invention relates to a human normal hepatocyte expression gene
 CC group comprising 200 genes in the human normal hepatocyte. The
 CC cDNA of each gene comprises one of 200 fully defined nucleotide
 CC sequences as given in the specification. The gene group and the cDNAs
 CC corresponding to each of the genes in the group are useful in the
 CC diagnosis and treatment of human hepatopathy. The present sequence
 CC is a cDNA corresponding to a gene expressed by normal human
 CC hepatocytes.
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
 XX
 QY Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 7 GCCAGGCCAA 16
    ||| |||||
Db 10 GCCTGGCCAA 1

RESULT 94
AAH76342/c
ID AAH76342 standard; DNA; 10 BP.
XX
AC AAH76342;
XX
DT 29-OCT-2001 (first entry)
XX
DE Z. mays Ms45 promoter deletion mutant fragment LS02.
XX
KM Ms45; male tissue; regulatory region; transcription; male fertility;
KM hybrid seed; promoter; ss.
XX
OS Zea mays.
XX
PN WO200160997-A2.
XX
PD 23-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-US04527.
XX
PR 15-FEB-2000; 2000US-0504487.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX
DR WPI; 2001-514772/56.
XX
PT A male tissue-preferred regulatory region comprising nucleotide
PT sequences essential for initiating transcription of the Ms45 gene
PT useful for mediating fertility in a male plant -
XX
PS Example 5; Fig 8; 50pp; English.
XX
CC The invention provides a male tissue-preferred regulatory region (I)
CC comprising nucleotide sequences essential for initiating transcription
CC of the Ms45 gene. A method of mediating male fertility in a plant is
CC provided that involves introducing an expression vector comprising a
CC promoter operably linked to (I) into a plant where the exogenous gene
CC impacts male fertility of the plant and (I) controls expression of the
CC exogenous gene. A method of producing hybrid seeds is also provided.
CC Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
CC promoter region, used for determining the essential region of Ms45
CC promoter.
XX
SQ Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 CGGGCCAGGC 13
    ||||| |||
Db 10 CGGGCCCGGC 1

RESULT 95
AAH76345
ID AAH76345 standard; DNA; 10 BP.
XX
AC AAH76345;
XX
DT 29-OCT-2001 (first entry)
XX
DE Z. mays Ms45 promoter deletion mutant fragment LS05.
XX

```

```

XX
KM Ms45; male tissue; regulatory region; transcription; male fertility;
KM hybrid seed; promoter; ss.
XX
OS Zea mays.
XX
PN WO200160997-A2.
XX
PD 23-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-US04527.
XX
PR 15-FEB-2000; 2000US-0504487.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX
DR WPI; 2001-514772/56.
XX
PT A male tissue-preferred regulatory region comprising nucleotide
PT sequences essential for initiating transcription of the Ms45 gene
PT useful for mediating fertility in a male plant -
XX
PS Example 5; Fig 8; 50pp; English.
XX
CC The invention provides a male tissue-preferred regulatory region (I)
CC comprising nucleotide sequences essential for initiating transcription
CC of the Ms45 gene. A method of mediating male fertility in a plant is
CC provided that involves introducing an expression vector comprising a
CC promoter operably linked to (I) into a plant where the exogenous gene
CC impacts male fertility of the plant and (I) controls expression of the
CC exogenous gene. A method of producing hybrid seeds is also provided.
CC Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
CC promoter region, used for determining the essential region of Ms45
CC promoter.
XX
SQ Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 CGGGCCAGGC 13
    ||||| |||
Db 1 CGGGCCCGGC 10

RESULT 96
AAH76348/c
ID AAH76348 standard; DNA; 10 BP.
XX
AC AAH76348;
XX
DT 29-OCT-2001 (first entry)
XX
DE Z. mays Ms45 promoter deletion mutant fragment LS08.
XX
KM Ms45; male tissue; regulatory region; transcription; male fertility;
KM hybrid seed; promoter; ss.
XX
OS Zea mays.
XX
PN WO200160997-A2.
XX
PD 23-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-US04527.
XX
PR 15-FEB-2000; 2000US-0504487.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX

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PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
 XX WPI; 2001-514772/56.
 XX
 XX
 PT A male tissue-preferred regulatory region comprising nucleotide
 PT sequences essential for initiating transcription of the MS45 gene
 PT useful for mediating fertility in a male plant -
 XX
 XX Example 5; Fig 8; 50pp; English.
 XX
 CC The invention provides a male tissue-preferred regulatory region (I)
 CC comprising nucleotide sequences essential for initiating transcription
 CC of the MS45 gene. A method of mediating male fertility in a plant is
 CC provided that involves introducing an expression vector comprising a
 CC promoter operably linked to (I) into a plant where the exogenous gene
 CC impacts male fertility of the plant and (i) controls expression of the
 CC exogenous gene. A method of producing hybrid seeds is also provided.
 CC Sequences AAH76341-355 represent a series of 5' deletions in the MS45
 CC promoter region, used for determining the essential region of MS45
 CC promoter.
 CC
 SQ Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;
 QY
 Db 5 GGGCCAGGCC 14
 10 GGGCCCGGCC 1
 RESULT 97
 AAH63580/c
 ID AAH63580 standard; cDNA; 10 BP.
 XX
 AC AAH63580;
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 420.
 XX
 KW Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 OS
 XX Homo sapiens.
 XX
 PN WO200138577-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 21-NOV-2000; 2000WO-US31922.
 XX
 PR 24-NOV-1999; 99US-0448480.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu VE, Vogelstein B, Kinzler KW;
 XX
 DR WPI; 2001-367706/38.
 XX
 PT New isolated polynucleotides, useful for identifying specific cell
 PT type, such as cancer cell, comprises transcriptomes expressed in
 PT particular cell types -
 XX
 PS Claim 13; Page 48; 94pp; English.
 XX
 CC The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences
 CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
 CC in the invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of
 CC the transcriptomes described in the exemplification of the invention.
 CC
 SQ Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;
 QY
 Db 5 GGGCCAGGCC 14
 10 GGGCCCGGCC 1
 RESULT 97
 AAH63580/c
 ID AAH63580 standard; cDNA; 10 BP.
 XX
 AC AAH63580;
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 420.
 XX
 KW Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 OS
 XX Homo sapiens.
 XX
 PN WO200138577-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 21-NOV-2000; 2000WO-US31922.
 XX
 PR 24-NOV-1999; 99US-0448480.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu VE, Vogelstein B, Kinzler KW;
 XX
 DR WPI; 2001-367706/38.
 XX
 PT New isolated polynucleotides, useful for identifying specific cell
 PT type, such as cancer cell, comprises transcriptomes expressed in
 PT particular cell types -
 XX
 PS Claim 13; Page 48; 94pp; English.
 XX
 CC The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences
 CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
 CC in the invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of
 CC the transcriptomes described in the exemplification of the invention.
 CC
 SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;
 QY
 Db 6 GGGCAGGCCA 15
 10 GGGCAGGCCA 1
 RESULT 99
 AAH63582
 ID AAH63582 standard; cDNA; 10 BP.
 XX

CC function of a diseased cell or tissue. The present sequence is one of
 CC the transcriptomes described in the exemplification of the invention.
 XX
 SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;
 QY
 Db 6 GGGCAGGCCA 15
 10 GGGCAGGCCA 1
 RESULT 98
 AAH63581/c
 ID AAH63581 standard; cDNA; 10 BP.
 XX
 AC AAH63581;
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 421.
 XX
 KW Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 OS
 XX Homo sapiens.
 XX
 PN WO200138577-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 21-NOV-2000; 2000WO-US31922.
 XX
 PR 24-NOV-1999; 99US-0448480.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu VE, Vogelstein B, Kinzler KW;
 XX
 DR WPI; 2001-367706/38.
 XX
 PT New isolated polynucleotides, useful for identifying specific cell
 PT type, such as cancer cell, comprises transcriptomes expressed in
 PT particular cell types -
 XX
 PS Claim 13; Page 48; 94pp; English.
 XX
 CC The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences
 CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
 CC in the invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of
 CC the transcriptomes described in the exemplification of the invention.
 CC
 SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;
 QY
 Db 6 GGGCAGGCCA 15
 10 GGGCAGGCCA 1
 RESULT 99
 AAH63582
 ID AAH63582 standard; cDNA; 10 BP.
 XX

AC AAH6382;
XX
XX
DT 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 422.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000WO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR
XX
XX (UYUO) UNIV JOHNS HOPKINS.
PA
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
DR
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
PS
XX
XX Claim 13; Page 48; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
XX
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;
XX
XX
XX Query Match 42.0%; Score 8.4; DB 1; Length 10;
XX Best Local Similarity 90.0%; Pred. No. 87;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 11 GGCCAAAGTC 20
QY |||||
DB 1 GGCCAAAGC 10
XX
XX
XX RESULT 100
XX AAH63804
ID AAH63804 standard; cDNA; 10 BP.
XX
XX AAH63804;
AC
XX
XX 20-SEP-2001 (first entry)
DT
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 644.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000WO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR

XX
XX (UYUO) UNIV JOHNS HOPKINS.
PA
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
DR
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
PS
XX
XX Claim 13; Page 53; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
XX
SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 other;
XX
XX
XX Query Match 42.0%; Score 8.4; DB 1; Length 10;
XX Best Local Similarity 90.0%; Pred. No. 87;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 10 AGGCCAAAGT 19
QY |||||
DB 1 AGGCCAAAGT 10
XX
XX
XX RESULT 101
XX AAH64388/c
ID AAH64388 standard; cDNA; 10 BP.
XX
XX AAH64388;
AC
XX
XX 20-SEP-2001 (first entry)
DT
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1228.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000WO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR
XX
XX (UYUO) UNIV JOHNS HOPKINS.
PA
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
DR
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
PS
XX
XX Claim 13; Page 67; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce

CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcripts described in the exemplification of the invention.
XX

Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCCAA 16
DB 10 GCCTGGCCAA 1

RESULT 102
AAH64389/C
ID AAH64389 standard; cDNA; 10 BP.

XX AAH64389;

XX 20-SEP-2001 (first entry)

XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1229.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KM cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US31922.

XX 24-NOV-1999; 99US-0448480.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcripts expressed in
PT particular cell types -

XX Claim 13; Page 67; 94pp; English.

XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcripts described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcripts described in the exemplification of the invention.

XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCCAA 16
DB 10 GCCTGGCCAA 1

RESULT 103
AAH64390/C
ID AAH64390 standard; cDNA; 10 BP.

XX AAH64390;
AC
XX 20-SEP-2001 (first entry)

XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1230.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KM cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US31922.

XX 24-NOV-1999; 99US-0448480.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcripts expressed in
PT particular cell types -

XX Claim 13; Page 67; 94pp; English.

XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcripts described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcripts described in the exemplification of the invention.

XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCCAA 16
DB 10 GCCTGGCCAA 1

RESULT 104

AAH64391/C
ID AAH64391 standard; cDNA; 10 BP.

XX AAH64391;

XX 20-SEP-2001 (first entry)

XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1231.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KM cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US31922.

PR 24-NOV-1999; 99US-0448480.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcripts expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 67; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcripts described
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcripts described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCCAGGCCAA 16
DB 10 GCCTGGCCAA 1
RESULT 105
AAH64392/c
ID AAH64392 standard; cDNA; 10 BP.
XX
XX AAH64392;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1232.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000WO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
DR
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcripts expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 67; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcripts described
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcripts described in the exemplification of the invention.
XX

CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcripts described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCCAGGCCAA 16
DB 10 GCCTGGCCAA 1
RESULT 106
AAH64393/c
ID AAH64393 standard; cDNA; 10 BP.
XX
XX AAH64393;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1233.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000WO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
DR
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcripts expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 67; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcripts described
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcripts described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCCAGGCCAA 16
DB 10 GCCTGGCCAA 1
RESULT 107
AAH64394/c

ID AAH64394 standard; cDNA; 10 BP.
XX
XX
AC AAH64394;
XX
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1234.
XX
KM Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000MO-US31922.
XX
PR 24-NOV-1999; 99US-0448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX
PS Claim 13; Page 67; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
XX
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 7 GCCAGGCCAA 16
Db 10 GCCTGGCCAA 1
XX
RESULT 108
AAH32882/c
ID AAH32882 standard; cDNA; 10 BP.
XX
AC AAH32882;
XX
DT 13-AUG-2001 (first entry)
XX
DE LPS activated human monocyte expression gene cDNA tag SEQ:255.
XX
KM Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
XX expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.
XX
PN JP2001069993-A.
XX
PD 21-MAR-2001.
XX
PF 28-APR-2000; 2000JP-0131079.
XX

XX
PR 08-JUL-1999; 99JP-0195103.
XX
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX
DR WPI; 2001-304369/32.
XX
PT LPS activated human monocyte expression gene group -
XX
PS Claim 19; Page 42; 52pp; Japanese.
XX
XX
CC The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence
CC 5'-CATG-3' nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role.
CC AAH32628 to AAH32943 represent specifically claimed LPS activated human
CC monocyte expression gene cDNA tags from the present invention. AAH32944
CC represents an LPS activated human monocyte expression gene cDNA sequence
CC encoding AAB98009, which are given in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;
XX
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 GGCGCAGGCC 14
Db 10 GTGCCAGGCC 1
XX
RESULT 109
AAF74058/c
ID AAF74058 standard; DNA; 10 BP.
XX
AC AAF74058;
XX
DT 30-APR-2001 (first entry)
XX
DE Human SLC6A4 allele-specific oligonucleotide primer #178.
XX
DE Solute carrier family 6 neurotransmitter transporter, section 4;
XX SLC6A4; genotyping; allele specific oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200109161-A1.
XX
PD 08-FEB-2001.
XX
PF 31-JUL-2000; 2000MO-US20638.
XX
PR 29-JUL-1999; 99US-0146290.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
XX
DR WPI; 2001-123317/13.
XX
PT New isolated polynucleotide comprising a polymorphic variant for the
PT solute carrier family 6 neurotransmitter transporter, serotonin member
PT 4 gene for identifying drugs for treating disorders related to
XX expression of the protein -
XX
PS Disclosure; Page 23; 152pp; English.
XX
CC The present invention relates to a polymorphic variant of a reference
XX

CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 6 GGCCAGGCCA 15
Db 10 GGCCAGGCCA 1
RESULT 112
AAF34406/c
ID AAF34406 standard; DNA: 10 BP.
XX
AC AAF34406;
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1145.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; de.
XX
OS Saccharomyces cerevisiae.
XX
PN MO200077214-A2.
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000MO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
PT MPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
XX Example; Page 40; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a

CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 6 GGCCAGGCCA 15
Db 10 GGCCAGGCCA 1
RESULT 113
AAF35939/c
ID AAF35939 standard; DNA: 10 BP.
XX
AC AAF35939;
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2678.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; de.
XX
OS Saccharomyces cerevisiae.
XX
PN MO200077214-A2.
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000MO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
PT MPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
XX Example; Page 95; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10⁴ between any two phases of the cell cycle selected from log
CC phase S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC gene may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF4064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
CC
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 11 GGCCAAAGTC 20
Db 10 GGCCAAAGTC 1
RESULT 114
AAFA1896/c
ID AAF41896 standard; DNA; 10 BP.
AC AAF41896;
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8635.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; de.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000MO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 308; 419p; English.
XX
CC The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10⁴ between any two phases of the cell cycle selected from log
CC phase S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC gene may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF4064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
CC
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 11 GGCCAAAGTC 20
Db 10 GGCCAAAGTC 1
RESULT 115
AAFA2385
ID AAF42385 standard; DNA; 10 BP.
AC AAF42385;
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9124.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; de.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000MO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -

XX Example; Page 325; 419pp; English.
PS
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 U; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 7 GCCAGGCCAA 16
1 GCCAGGCCAA 10
RESULT 116
AAAF3779/c
ID AAF43779 standard; DNA; 10 BP.
XX
AC AAF43779;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11918.
XX
KM Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
KM serial analysis of gene expression; antifungal; tag; identification;
KM linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000MO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 375; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 7 GCCAGGCCAA 16
10 GCCAGGCCAA 1
RESULT 117
ABV84222
ID ABV84222 standard; cDNA; 10 BP.
XX
AC ABV84222;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human heat shock protein 40 (HSP40-1) SAGE tag #32.
XX
KM SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KM CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KM expression pattern; differential expression; ss.
XX
OS Homo sapiens.
XX
PN JP2002209591-A.
XX
PD 30-JUL-2002.
XX
PF 19-JAN-2001; 2001JP-0012328.
XX
PR 19-JAN-2001; 2001JP-0012328.
XX
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX

DR WPI; 2002-631294/68.
XX Human chronic hepatitis C tissue expression exasperating gene group
PT comprises 100 high-ranking genes -
XX
PS Claim 1; Page 10; 139pp; Japanese.
XX
CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the
CC pattern of gene expression in particular cell types. The invention also
CC relates to proteins encoded by the genes expressed in chronic hepatitis
CC C liver tissue or HCC, antibodies against these proteins, and inhibitors
CC of the expression of groups of genes that are overexpressed in chronic
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC treatment of these diseases. Such genes, inhibitors of their expression
CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC ABV84591-ABV84290 are SAGE tags representing the 100 most highly
CC expressed genes out of those genes which are overexpressed in chronic
CC hepatitis C liver tissue compared with normal liver tissue.
XX
SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 other;
XX
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 10 AGGCCCAAGT 19
DB 1 AGGCCCAAGT 10
XX
RESULT 118
ABV84641/c
ID ABV84641 standard; cDNA; 10 BP.
XX
AC ABV84641;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human HCC/chronic hepatitis C differentially expressed EST SAGE tag #451.
XX
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; differential expression; EST; expressed sequence tag;
SS.
XX
OS Homo sapiens.
XX
PN JP2002209591-A.
XX
PD 30-JUL-2002.
XX
PF 19-JAN-2001; 2001JP-0012328.
XX
PR 19-JAN-2001; 2001JP-0012328.
XX
PS (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-631294/68.
XX
PT Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes -
XX
PS Claim 37; Page 23; 139pp; Japanese.
XX

CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the
CC pattern of gene expression in particular cell types. The invention also
CC relates to proteins encoded by the genes expressed in chronic hepatitis
CC C liver tissue or HCC, antibodies against these proteins, and inhibitors
CC of the expression of groups of genes that are overexpressed in chronic
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC treatment of these diseases. Such genes, inhibitors of their expression
CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC ABV84591-ABV84690 are SAGE tags representing the 100 most highly
CC expressed genes out of those genes which are overexpressed in
CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue.
XX
SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 other;
XX
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 10 AGGCCCAAGT 19
DB 10 AGGCCCAAGT 1
XX
RESULT 119
ABV84947/c
ID ABV84947 standard; cDNA; 10 BP.
XX
AC ABV84947;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human multiple HCC highly expressed genes SAGE tag #757.
XX
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; ss.
XX
OS Homo sapiens.
XX
PN JP2002209591-A.
XX
PD 30-JUL-2002.
XX
PF 19-JAN-2001; 2001JP-0012328.
XX
PR 19-JAN-2001; 2001JP-0012328.
XX
PS (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-631294/68.
XX
PT Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes -
XX
PS Claim 64; Page 31; 139pp; Japanese.
XX
CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the

CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis
 CC C liver tissue or HCC, antibodies against these proteins, and inhibitors
 CC of the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
 CC expressed in hepatocellular carcinoma.

XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCCAA 16
 DB 10 GCCAGGCCAA 1

RESULT 120
 ABV78373/c

ID ABV78373 standard; cDNA; 10 BP.

XX ABV78373;

DT 29-NOV-2002 (first entry)

DE Human Th2 cell SAGE tag, SEQ ID NO:84.

XX SAGE tag: serial analysis of gene expression; human; Th2 cell;

KM activated T cell; T lymphocyte; immune response; expression pattern;

XX immune disorder; ss.

OS Homo sapiens.

XX JP2002186482-A.

PD 02-JUL-2002.

PF 19-DEC-2000; 2000JP-0385816.

XX 19-DEC-2000; 2000JP-0385816.

PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.

XX WPI; 2002-594261/64.

PT Human activated Th1 and Th2 cell expression gene group, useful for the

PT diagnosis and treatment of Th1 and Th2-related diseases -

PS Claim 10; Page 9; 60pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are expressed in activated human Th1
 CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
 CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
 CC lying nearest to the polyA region of cDNAs derived from a variety of
 CC genes. These tags serve to uniquely identify each transcript and can thus
 CC be used to analyse the pattern of gene expression in particular cell
 CC types. The invention also relates to proteins encoded by the genes
 CC expressed in Th1 and/or Th2 cells, antibodies against these proteins,
 CC and inhibitors of the expression of groups of genes that are expressed
 CC in either or both the two cell types. Groups of genes expressed in Th1
 CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
 CC and Th2-related disorders. Sequences ABV78340-ABV78389 are SAGE tags
 CC representing 50 genes which are most highly expressed in Th2 cells.

XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCCAA 16
 DB 10 GCCAGGCCAA 1

RESULT 121

ABK95837
 ID ABK95837 standard; DNA; 10 BP.

XX ABK95837;

DT 24-SEP-2002 (first entry)

DE Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #8.

XX Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;

KM glutamate/neutral amino acid transporter; neurological disease; PCR; ss;

XX amino acid transporter disorder; single nucleotide polymorphism; SNP.

OS Homo sapiens.

XX WO200244198-A2.

PD 06-JUN-2002.

PF 29-NOV-2001; 2001WO-US44781.

XX 30-NOV-2000; 2000US-250254P.

PA (GENA-) GENAISSANCE PHARM INC.

XX Bieganski KM, Kazemi A, Russo DP, Sausker EA,

XX WPI; 2002-519580/55.

PT Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral

PT Amino Acid Transporter), Member 4 isogenes, for improving efficiency

PT and reliability in drug development for treating cancers -

PS Claim 17; Page 16; 139pp; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
 CC first nucleotide sequence which comprises solute carrier family 1
 CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes
 CC (II) and an isolated polypeptide (III) comprising an amino acid sequence
 CC which is a polymorphic variant of a reference sequence for SLC1A4
 CC protein. Also described are methods for: (1) haplotyping or genotyping
 CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
 CC gene of an individual; (3) identifying an association between a trait and
 CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) is useful
 CC in screening for drugs targeting (III) that are useful for treating
 CC cancer, neurological diseases and amino acid transporter disorders. The
 CC methods are useful for improving the efficiency and reliability of
 CC several steps in the discovery and development of drugs for treating
 CC diseases associated with SLC1A4 activity. The haplotyping method is also
 CC used by the pharmaceutical research scientist to validate SLC1A4 as a
 CC candidate target for treating a specific condition or disease predicted
 CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
 CC and amino acid transporter disorders, and in the design of clinical
 CC trials for treating a specific condition of disease associated with
 CC SLC1A4 activity. The methods are also useful for screening compounds
 CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,
 CC prognostic and therapeutic methods. ABK95761-ABK95877 represent
 CC SLC1A4 gene allele-specific oligonucleotides, primer extension
 CC oligonucleotides and related PCR primers used to identify single
 CC nucleotide polymorphisms (SNP) of the gene.

XX Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGG 12
 |||||
 1 CCGGGCCCTGG 10

RESULT 122

ABK95838
 ID ABK95838 standard; DNA; 10 BP.

XX
 AC ABK95838;

XX
 DT 24-SEP-2002 (first entry)

XX
 DE Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #9.

XX
 KM Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
 KM glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
 KM amino acid transporter disorder; single nucleotide polymorphism; SNP.

XX
 OS Homo sapiens.

XX
 PN WO20024198-A2.

XX
 PD 06-JUN-2002.

XX
 PF 29-NOV-2001; 2001WO-US44781.

XX
 PR 30-NOV-2000; 2000US-250254P.

XX
 PA (GENA-) GENAISSANCE PHARM INC.

XX
 PI Bieglecki KM, Kazemi A, Russo DP, Sausker EA;

XX
 DR WPI; 2002-519580/55.

XX
 PT Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
 PT Amino Acid Transporter), Member 4 isogenes, for improving efficiency
 PT and reliability in drug development for treating cancers -

XX
 PS Claim 17; Page 16; 139pp; English.

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGCC 14
 |||||
 1 CCGCCAGGCC 10

RESULT 123

ABA97040/c
 ID ABA97040 standard; DNA; 10 BP.

XX
 AC ABA97040;

XX
 DT 18-JUN-2002 (first entry)

XX
 DE ZFP36 extension primer for detecting polymorphisms SEQ ID 41.

XX
 KM Polymorphic variant; ZFP36; immunosuppressive; antirheumatic;
 KM antirheumatic; drug screening; isogene; haplotype pair;
 KM autoimmune disease; rheumatoid arthritis; haplotyping; genotyping;
 KM allele specific oligonucleotide; ASO; single nucleotide polymorphism;
 KM SNP; zinc finger protein; mouse zfp-36; ss; gene therapy; transgenic;
 KM primer.

XX
 OS Homo sapiens.

XX
 PN WO200179226-A2.

XX
 PD 25-OCT-2001.

XX
 PF 13-APR-2001; 2001WO-US12254.

XX
 PR 13-APR-2000; 2000US-196602P.

XX
 PA (GENA-) GENAISSANCE PHARM INC.

XX
 PI Choi JY, Kiem SE, Koshy B, Parks KE;

XX
 DR WPI; 2002-075059/10.

XX
 PT Novel polymorphic variants of zinc finger protein homologous to zfp-36
 PT in mouse gene, useful in studying expression and function of the
 PT protein, useful for screening drugs to treat diseases e.g. rheumatoid
 PT arthritis -

XX
 PS Claim 18; Page 14; 60pp; English.

XX
 CC The present sequence is that of an oligonucleotide used for assaying a
 CC polymorphism in the zinc finger protein homologous to zfp-36 in mouse
 CC (ZFP36) gene of the invention. The specification describes a newly
 CC isolated polynucleotide comprising a sequence which is a polymorphic
 CC variant (PV) of a reference sequence for the ZFP36 gene (see ABA97001) or
 CC its fragment and its encoded protein. The ZFP36 polynucleotides and
 CC polypeptides have antirheumatic, immunosuppressive and antirheumatic
 CC activities. The ZFP36 polypeptide is useful for screening drugs targeting
 CC the ZFP36 polypeptide. ZFP36 isogenes or haplotype pairs are useful for
 CC improving the efficiency and reliability of the discovery and development
 CC of drugs for treating diseases associated with ZFP36 activity, e.g.,
 CC autoimmune diseases such as rheumatoid arthritis. Haplotyping the ZFP36
 CC gene in an individual gives useful information for validating ZFP36 as a
 CC candidate target for treating a specific condition predicted to be
 CC associated with ZFP36 activity. Genotyping the ZFP36 gene of an
 CC individual can give information used for developing diagnostic tests and
 CC therapeutic treatments. The isolated polynucleotide is useful in studying
 CC the expression and function of ZFP36 and in drug screening. Antibodies
 CC specific for the ZFP36 protein are useful in many diagnostic and
 CC prognostic formats and therapeutic methods. A recombinant non-human
 CC organism transformed with the ZFP36 gene is useful in studying expression
 CC of the ZFP36 isogenes in vivo, for in vivo drug screening and testing.
 CC Allele-specific oligonucleotides (ASO) are useful as probes and primers
 CC and for assaying a polymorphism in the target region.

XX
 CC Sequence 10 BP; 1 A; 5 C; 4 G; 0 U; 0 other;

XX Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 other;
 SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 GCGGCCAGGC 13
 Db 10 CCGGCCAGGC 1

RESULT 124
 ABK64054/c
 ID ABK64054 standard; DNA; 10 BP.
 XX
 AC ABK64054;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human BF gene allele-specific oligonucleotide PCR primer #5.
 XX
 KM Human; B-factor; properdin; BF; primer; ss; gene therapy; drug screening;
 KM antidiabetic; dermatological; diabetes; immunosuppressive;
 KM antiinflammatory; systemic lupus erythematosus.
 XX
 OS Homo sapiens.
 XX
 PN WO200218414-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 29-AUG-2001; 2001WO-US27098.
 XX
 PR 29-AUG-2000; 2000US-228940P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Anastasio AE, Finkel K, Kazemi A, Koshy B;
 XX
 DR WPI; 2002-304244/34.
 XX
 PT New genetic variants having polymorphisms in the B-Factor, Properdin
 PT (BF) gene, useful for studying the function of BF, and for treating
 PT disorders affected by expression or function of the BF isogene
 XX
 PS Claim 19; Page 16; 151pp; English.
 XX
 CC The invention relates to single nucleotide polymorphisms in the gene
 CC encoding the human B-factor properdin protein (BF). A method for
 CC haplotyping the BF gene in an individual comprises identifying the
 CC nucleotide at one or more polymorphic sites and determining whether one
 CC of the copies of the gene is defined by one of the BF haplotypes given in
 CC the specification or whether both copies are defined by a haplotype pair.
 CC This method is useful in genotyping, whereby all possible haplotype pairs
 CC can be assigned to specific genotypes. An association between a trait and
 CC a haplotype or haplotype pair of the BF gene can be identified by
 CC comparing the frequency of the haplotype or haplotype pair in a
 CC population exhibiting the trait with the frequency of the haplotype or
 CC haplotype pair in a reference population, where a higher haplotype or
 CC frequency in the trait population indicates the trait is associated with
 CC the haplotype or haplotype pair. BF and its corresponding DNA are used
 CC for studying the expression and function of BF, for use in screening for
 CC candidate drugs to treat diseases related to BF activity, such as
 CC diabetes and systemic lupus erythematosus. Sequences ABK64050-ABK64105
 CC represent allele-specific PCR primers used to detect human BF gene
 CC polymorphisms.
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 other;
 XX
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GGCCAAAGTC 20
 Db 10 GGCCAAAGAC 1

RESULT 125
 AAS19876
 ID AAS19876 standard; DNA; 10 BP.
 XX
 AC AAS19876;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Oligonucleotide #56 to detect human RANGAP1 gene polymorphisms.
 XX
 KM Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping
 KM chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
 KM cancer; irregular cell cycle associated disorder; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200179240-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US12455.
 XX
 PR 17-APR-2000; 2000US-198072P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Choi JY, Koshy B;
 XX
 DR WPI; 2002-075068/10.
 XX
 PT Genotyping human Ran GTPase activating protein 1 gene of individual for
 PT determining haplotype of individual, involves determining identity of
 PT nucleotide pair at specific polymorphic sites for two copies of the
 XX
 PS Claim 17; Page 16; 148pp; English.
 XX
 CC The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
 CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
 CC genotyping the RANGAP1 gene. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the RANGAP1 gene
 CC polymorphisms. The polymorphisms and screened compounds are useful for
 CC treatment of diseases associated with RANGAP1 activity, such as
 CC cancer and other disorders associated with an irregular cell cycle.
 CC AAS19821-AAS19898 represent primer-extension oligonucleotides for
 CC detecting human RANGAP1 gene polymorphisms.
 XX
 SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;
 XX
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 GGCACAGCCA 15
 Db 1 GGCCAGAC 10

RESULT 126
 ABK23567/c
 ID ABK23567 standard; DNA; 10 BP.
 XX
 AC ABK23567;
 XX
 DT 09-APR-2002 (first entry)

```

XX XX Transcript tag DNA sequence #156 induced or suppressed by N-myc.
DE XX
XX XX Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KM XX spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KM myc oncogene; N-myc; human neuroblastoma; cytosolic; ds.
XX XX
OS Homo sapiens.
XX XX
XX XX MO200185941-A2.
XX XX
XX XX 15-NOV-2001.
XX XX
XX PF 11-MAY-2001; 2001MO-NL00361.
XX XX
XX PR 11-MAY-2000; 2000EP-0201698.
XX PR 29-JUN-2000; 2000EP-0202284.
XX XX
XX PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX XX
XX PI Versteeg R, Caron HN;
XX XX
XX DR WPI; 2002-066603/09.
XX XX
XX PT A new nucleic acid library of myc-dependent downstream genes capable of
PT supporting a neoplastic characteristic of cancer is useful to find new
PT therapies and diagnoses for cancer.
XX XX
XX PS Disclosure; Page 53; 69pp; English.
XX XX
XX CC The present invention relates to a nucleic acid library comprising
XX CC myc-dependent downstream genes or their functional fragments essentially
XX CC capable of supporting a neoplastic character of cancer such as growth,
XX CC invasion or spread. These myc target or tag sequences are identified
XX CC by SAGE (serial analysis of gene expression). The library is useful to
XX CC find new diagnoses and treatments for cancer. The invention is also
XX CC useful to enhance production of recombinant proteins in a production
XX CC system with high expression of endogenous or transfected myc oncogenes.
XX CC ABK2412-ABK2328 represent transcript tag DNA sequences that are
XX CC activated or repressed by N-myc in human neuroblastoma.
XX XX
XX SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;
XX XX
XX Query Match 42.0%; Score 8.4; DB 1; Length 10;
XX Best Local Similarity 90.0%; Pred. No. 87;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
OY 6 GGCCAGGCCA 15
DB 10 GGCCAGGCCA 1
XX XX
XX RESULT 127
XX ABK24232
XX ID ABK24232 standard; DNA; 10 BP.
XX AC ABK24232;
XX XX
XX 09-APR-2002 (first entry)
XX XX
XX DE Retinaldehyde-binding protein 1 ASO primer extension primer #5.
XX XX
XX KM Human; retinaldehyde-binding protein 1; ser; RIBP1; haplotype; primer;
XX KM genotyping; probe; autosomal recessive retinitis pigmentosa; arRP; PCR;
XX KM chromosome 15q26; transgenic; ASO; allele specific oligonucleotide.
XX XX
XX OS Homo sapiens.
XX XX
XX PN MO200192278-A2.
XX XX
XX PD 06-DEC-2001.
XX XX
XX PF 29-MAY-2001; 2001MO-US17252.

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XX XX 26-MAY-2000; 2000US-207618P.
XX PR
XX XX (GENA-) GENAISSANCE PHARM INC.
XX PA
XX XX Choi JY, Kazemi A, Koshy B;
XX PI
XX XX WPI; 2002-122053/16.
XX XX
XX XX New genetic variants having polymorphisms in the retinaldehyde-binding
XX PT protein 1 gene, useful for studying the function of and for expressing
XX PT RIBP1 protein for use in screening drugs for treating diseases related
XX PT to RIBP1 activity.
XX XX
XX PS Claim 18; Page 14; 107pp; English.
XX XX
XX CC The invention relates to an isolated polynucleotide, which comprises
XX CC genes and haplotypes of the retinaldehyde-binding protein 1 (RIBP1) gene.
XX CC The polynucleotide comprises polymorphic sites in the RIBP1 gene, which
XX CC are referred to as P51-24 to designate the order in which they are
XX CC located in the gene. Also included are methods for haplotyping or
XX CC genotyping the RIBP1 gene of an individual, a method for predicting a
XX CC haplotype pair for the RIBP1 gene of an individual, a method for
XX CC identifying an association between a trait and at least one haplotype or
XX CC haplotype pair of the RIBP1 gene, a composition comprising at least one
XX CC genotyping oligonucleotide for detecting a polymorphism in the RIBP1 gene
XX CC at a PS consisting of P51-P524, a kit for genotyping the RIBP1 gene of an
XX CC individual comprising a set of oligonucleotides designed to genotype each
XX CC of P51-P524 recombinant non-human organisms transformed or transfected
XX CC with the isolated polynucleotide, where the organism expresses a RIBP1
XX CC protein encoded by the first nucleotide sequence or expresses an RIBP1
XX CC protein encoded by the polymorphic variant sequence, an isolated
XX CC polypeptide comprising an amino acid sequence that is a polymorphic
XX CC variant of a reference sequence for the RIBP1 protein or its fragment,
XX CC an anti-RIBP1 antibody, a method for screening for drugs targeting the
XX CC isolated polypeptide, and a computer system for storing and analysing
XX CC polymorphism data for the RIBP1 oncogene gene.
XX CC
XX CC The polynucleotide comprising polymorphisms in the RIBP1 gene is
XX CC useful in studying the expression and function of RIBP1, and in
XX CC expressing RIBP1 protein for use in screening candidate drugs to treat
XX CC diseases related to RIBP1 activity (e.g. autosomal recessive
XX CC retinitis pigmentosa (arRP)). The methods and haplotypes are
XX CC useful in improving the efficiency and output of several steps in the
XX CC drug discovery and development process, including target validation,
XX CC identifying lead compounds, and early phase clinical trials. These are
XX CC also useful for designing clinical trials of candidate drugs for
XX CC treating a specific condition or disease, as well as for screening
XX CC compounds targeting RIBP1 to treat a specific condition or disease
XX CC predicted to be associated with RIBP1 activity. The kit and method are
XX CC useful for determining whether an individual has one of the haplotypes
XX CC or haplotype pairs cited above. The transgenic animals are useful for
XX CC studying expression of the RIBP1 isogenes in vivo, for in vivo
XX CC screening and testing of drugs targeted against RIBP1 protein, and for
XX CC testing the efficacy of therapeutic agents and compounds for retinal
XX CC diseases in a biological system. The gene for RIBP1 is located on
XX CC chromosome 15q26. The present sequence is an allele specific
XX CC oligonucleotide (ASO) PCR primer for amplifying a nucleic acid containing
XX CC a polymorphic RIBP1 sequence, using the primer extension method.
XX XX
XX SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 U; 0 other;
XX XX
XX Query Match 42.0%; Score 8.4; DB 1; Length 10;
XX Best Local Similarity 90.0%; Pred. No. 87;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
OY 8 CCAGGCCAAA 17
DB 1 CCAGGCCAAG 10
XX XX
XX RESULT 128
XX AAS99275
XX ID AAS99275 standard; DNA; 10 BP.

```

XX AAS99275;
 AC 12-MAR-2002 (first entry)
 DT XX
 DE Human F12 gene allele-specific oligonucleotide PCR primer #2.
 XX
 KW Human; coagulation factor XII; F12; haplotyping; haplotype pair; ss;
 KW single nucleotide polymorphism; genotyping; gene therapy; drug screening;
 KW coronary artery disease; liver disease; spontaneous abortion; cardiac;
 KW Alzheimer's disease; blood coagulation; hepatotropic; neuroprotective;
 KW nototropic; coagulant; antiabortive; sequencing primer; PCR primer; probe;
 KW primer tail.
 OS Homo sapiens.
 XX WO200179228-A2.
 XX
 PN 25-OCT-2001.
 XX
 PD 13-APR-2001; 2001WO-US12257.
 XX
 PF 14-APR-2000; 2000US-197837P.
 XX
 PR (GENA-) GENAISSANCE PHARM INC.
 XX
 PA Bentivegna SC, Chew A, Choi JY, Nandabalan K;
 XX
 PI WPI; 2002-075061/10.
 XX
 DR Novel isolated human coagulation factor XII polynucleotide, F12 useful
 XX for treatment of e.g. coronary artery disease, comprises a sequence
 PT which is a polymorphic variant of a reference sequence for F12 gene or
 PT its fragment -
 XX
 PS Claim 18; Page 14; 72pp; English.
 XX
 CC The invention relates to single nucleotide polymorphisms in the gene
 CC encoding the human coagulation factor XII (F12) polypeptide. A method for
 CC haplotyping the F12 gene in an individual comprises identifying the
 CC nucleotide at one or more polymorphic sites and determining whether one
 CC of the copies of the gene is defined by one of the F12 haplotypes given
 CC in the specification or whether both copies are defined by a haplotype
 CC pair. This method is useful in genotyping, whereby all possible haplotype
 CC pairs can be assigned to specific genotypes. An association between a
 CC trait and a haplotype or haplotype pair of the F12 gene can be identified
 CC by comparing the frequency of the haplotype or haplotype pair in a
 CC population exhibiting the trait with the frequency of the haplotype or
 CC haplotype pair in a reference population, where a higher haplotype
 CC frequency in the trait population indicates the trait is associated with
 CC the haplotype or haplotype pair. F12 and its corresponding DNA are used
 CC for studying the expression and function of F12, for use in screening for
 CC candidate drugs to treat disorders related to F12 activity such as
 CC coronary artery disease, liver disease, spontaneous abortion, Alzheimer's
 CC disease and other diseases associated with defects in blood coagulation.
 CC The sequences are also useful for studying the effect of variation on the
 CC biological activity of F12 as well as on the binding affinity of
 CC candidate drugs targeting F12. Sequences AAS99229-AAS99305 represent
 CC probes, primers and primer tails used to detect F12 gene polymorphisms.
 CC
 XX Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 other;
 SQ

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CAGGCCAAG 18
 | |||||
 DB 1 CTGGCCAAAG 10

RESULT 129
 AAS16750/c

ID AAS16750 standard; DNA; 10 BP.
 XX
 AC AAS16750;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human APOA4 ASO, primer extension primer #3 terminal sequence.
 XX
 KW Human; ss; APOA4; apolipoprotein A-IV; atherosclerotic; cardiac;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
 KW atherosclerosis; PCR primer; primer extension.
 XX
 OS Homo sapiens.
 XX WO200177124-A2.
 XX
 PN 18-OCT-2001.
 XX
 PD 03-APR-2001; 2001WO-US10670.
 XX
 PF 05-APR-2000; 2000US-194362P.
 XX
 PR (GENA-) GENAISSANCE PHARM INC.
 XX
 PA Bentivegna SC, Choi JY, Kiem SE, Koshy B;
 XX
 PI WPI; 2002-041281/05.
 XX
 DR New haplotypes of the human apolipoprotein A-IV gene, useful to
 XX diagnose and treat disorders associated with its abnormal expression or
 PT function such as coronary artery disease -
 PT
 PS Claim 17; Page 15; 71pp; English.
 XX
 CC The invention relates to haplotyping the human apolipoprotein A-IV
 CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or
 CC allele specific oligonucleotides, ASO) as well as methods for correlating
 CC a particular haplotype pair with a trait e.g. obesity, in a population.
 CC The APOA4 gene is located on chromosome 11q23-qter. The methods of the
 CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is the terminus of an APOA4 allele specific
 CC oligonucleotide, ASO, primer extension PCR primer used to detect an APOA4
 CC polymorphism.
 CC
 XX Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;
 SQ

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGCCAGG 12
 | |||||
 DB 10 CAGGCCAAG 1

RESULT 130
 ABL42671/c
 ID ABL42671 standard; cDNA; 10 BP.
 XX
 AC ABL42671;
 XX
 DT 12-APR-2002 (first entry)
 XX
 DE Human maturation/activation dendritic cell expression gene tag #45.
 XX
 KW Human; maturation/activation dendritic cell expression gene; tag;
 KW maturation; activation; dendritic cell; ss.

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XX OS Homo sapiens.
XX PN JP2001327293-A.
XX PD 27-NOV-2001.
XX PF 22-MAY-2000; 2000JP-0150562.
XX PR 22-MAY-2000; 2000JP-0150562.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 2002-127070/17.
XX PT Human maturation/activation dendritic cell expression gene group -
XX PS Claim 1; Page 9; 41pp; Japanese.
XX SQ The present invention describes a human maturation/activation dendritic
CC cell (DC) expression gene group consisting of 100 genes which show the
CC highest expression among the genes expressed in human maturation/
CC activation DC. Also described are: (1) a protein expressed by the above
CC human maturation/activation DC expression gene; (2) an antibody against
CC the protein; and (3) an antagonist against the expression of each gene
CC belonging to the above gene group. The gene group is useful for the
CC treatment and the diagnosis of various human diseases related to human
CC DC. ABU42627 to ABU42926 represent specifically claimed human
CC maturation/activation DC expression gene tags from the present invention.
XX SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCCAA 16
DB 10 GCCTGGCCAA 1

RESULT 131
ABV62380
ID ABV62380 standard; cDNA; 11 BP.
AC ABV62380;
XX 21-OCT-2002 (first entry)
XX DE Human skin EST 166.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP15179.
XX PR 03-JAN-2001; 2001DE-1000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against

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PT e.g. skin cancer -
XX XS Disclosure; Page 30; 1345pp; German.
XX PS The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders; specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX SQ Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 11e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 CCGGCGCAGG 12
DB 2 CCGGCCAGG 11

RESULT 132
ABV69801
ID ABV69801 standard; cDNA; 11 BP.
AC ABV69801;
XX 21-OCT-2002 (first entry)
XX DE Human skin EST 7587.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP15179.
XX PR 03-JAN-2001; 2001DE-1000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX XS Claim 24; Page 240; 1345pp; German.
XX PS The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders; specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

```

CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.

XX Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGCCGAGC 12
 |||||
 Db 2 CCGGCCGAGC 11

RESULT 133

AAK54916
 ID AAK54916 standard; DNA; 11 BP.

AC AAK54916;

DT 05-JUL-1999 (first entry)

DE C/EBP-beta antisense oligonucleotide fragment.

KM Antisense oligonucleotide; multiple target; antisense treatment;
 KM impaired respiration; inflammation; lung disease;

KM pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KM acute asthma; allergy; asthma; impeded respiration;

KM respiratory distress syndrome; pain; cystic fibrosis;
 KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;

KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KM colon cancer; breast cancer; lung cancer; pancreatic cancer;

KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KM prostate cancer; ss.

OS Synthetic.

PN WO913886-A1.

XX 25-MAR-1999.

PF 17-SEP-1998; 98WO-US19419.

PR 09-JUN-1998; 98US-0093972.

PR 17-SEP-1997; 97US-0059160.

XX (UYEC-) UNIV EAST CAROLINA.

PA NYCE JW;

PI WPI; 1999-229400/19.

DR New antisense oligonucleotides used in treatment of, e.g. pulmonary
 XX vasoconstriction

PT Disclosure; Page 68; 120pp; English.

XX The specification describes antisense oligonucleotides (AAK52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene

CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxtaposition between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides

CC may be derived from sequences AAK5272-74. These multiple target
 CC oligonucleotides (specifically AAK55180-271) can be used for the

CC antisense treatment of diseases and conditions. Typical diseases and
 CC conditions are those associated with impaired respiration and

CC inflammation, including lung diseases, pulmonary vasoconstriction,
 CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded

CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
 CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic

CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
 CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
 CC hepatic metastases, as well as all types of cancers which may metastasize
 CC or have metastasized to the lungs, including breast and prostate cancer.

XX Sequence 11 BP; 0 A; 4 C; 6 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCGGCCGAGC 13
 |||||
 Db 2 CCGGCCGAGC 11

RESULT 134

AAF20485
 ID AAF20485 standard; DNA; 11 BP.

AC AAF20485;

DT 14-MAR-2001 (first entry)

DE Human C/EBP polynucleotide fragment #2052.

KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;

KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antiallergic; analgesic; hypotensive; cytostatic;

KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;

KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;

KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.

OS Homo sapiens.

PN WO200062736-A2.

XX 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US08020.

PR 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PI NYCE JW;

DR WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -

XX Claim 14; Page 262; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense

CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,

CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the

CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and

CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and

CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and

CC

CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisease oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impaired respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisease oligonucleotides used in the exemplification of
CC the present invention.

SQ Sequence 11 BP; 0 A; 4 C; 6 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 CGGGCCGGC 11

RESULT 135

AAA34363 standard; DNA; 11 BP.

AAA34363;

28-JUL-2000 (first entry)

Human adenosine receptor related polynucleotide SEQ ID NO:2052.

Human; adenosine receptor; low adenosine antisease oligonucleotide;
phosphorothioate; impaired respiration; inflammation; allergy;
allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
antiallergic; antiasthmatic; cytosolic; analgesic; impaired airway;
lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
respiratory distress syndrome; pain; cystic fibrosis; emphysema;
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

MO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99MO-US17712.

03-AUG-1998; 98US-0095212.

(UYEC-) UNIV EAST CAROLINA.

Nyce JM;

WPI; 2000-205971/18.

New antisease oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -

Disclosure; Page 523; 1343pp; English.

The present invention describes a new composition comprising an
CC antisease oligonucleotide (ON) with low adenosine (up to 15%), which

CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytosolic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA2313 to AAA3312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA2323 to AAA3392) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

SQ Sequence 11 BP; 0 A; 4 C; 6 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 CGGGCCGGC 11

RESULT 136

AAZ59919/C standard; DNA; 11 BP.

AAZ59919;

08-MAY-2000 (first entry)

CouP-TF inverted repeat binding site.

CouP-TF binding site; inverted repeat; minimal packaging element;
KM adenovirus; chicken ovalbumin upstream promoter transcription factor;
KM repressor binding site; DNA delivery; recombinant virus; ds.

Nastadenovirus.

MO9953085-A2.

21-OCT-1999.

15-APR-1999; 99MO-US08294.

15-APR-1998; 98US-0081867.

05-JUN-1998; 98US-0088321.

(UYNY) UNIV NEW YORK STATE RES FOUND.

Hearing P, Schmid SI, Ostapchuk PH, Erturk E;

WPI; 2000-052657/04.

Regulating adenoviral packaging by incorporation of repressor binding
PT sites that allow selective suppression of packaging, used for gene
PT therapy -

Example 5; Page 39; 71pp; English.

The invention relates to the regulation of adenoviral packaging.

CC The method of the invention comprises propagating an adenoviral
 CC vector containing a repressor binding site, in the absence of the
 CC repressor. After propagation, vector packaging is repressed by the
 CC appropriate repressor protein. The invention also encompasses an
 CC adenoviral vector that includes an adenoviral packaging sequence
 CC containing several COUP-TF (chicken ovalbumin upstream promoter
 CC transcription factor) binding sites (AA25919). Adenoviral vectors
 CC containing repressor binding sites are used for DNA delivery, e.g., for
 CC expression of a therapeutic protein; in genetic immunisation; or to
 CC produce antiviral DNA or antisense RNA. Typical heterologous genes that
 CC can be expressed include those for interleukin-2, alpha-antitrypsin,
 CC cystic fibrosis transmembrane conductance regulator and coagulation
 CC factor VIII. These vectors have very large capacity (up to 36 Kb) for
 CC foreign DNA, and minimise the risk of generating replication competent
 CC virus (since vector and helper virus can be designed such that they
 CC have no overlapping packaging sequences that might permit homologous
 CC recombination). The presence of the repressor binding site allows
 CC selective inhibition of virion production (i.e., packaging of one vector
 CC in the presence of another). The present sequence represents a COUP-TF
 CC inverted repeat binding site. COUP-TF binds to the consensus sequence
 CC 5'-GGTCA-3' when situated as a direct or inverted repeat. These binding
 CC sites overlap the A repeat AVI sequence, with other A repeats contain
 CC similar sequence motifs. Binding of COUP-TF can specifically repress
 CC adenovirus packaging.

CC Sequence 11 BP; 2 A; 3 G; 3 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1,1e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

11 GGCCAAAGTC 20
 11 GGCCAAAGTC 2

RESULT 137
 ABQ81854
 ID ABQ81854 standard; DNA; 11 BP.

XX AC ABQ81854;

XX DT 19-NOV-2002 (first entry)

XX DE Kaposi's Sarcoma SAGE library Tag No.4 SEQ ID NO:4.

XX KM Human; Kaposi's sarcoma; tumour; angiogenesis; tag; ss.

XX OS Homo sapiens.

XX PN EP1225233-A2.

XX PD 24-JUL-2002.

XX PF 23-JAN-2002; 2002EP-0075264.

XX PR 23-JAN-2001; 2001EP-0200228.

XX PR 28-SEP-2001; 2001EP-0203703.

XX PR 28-SEP-2001; 2001US-325722P.

XX PA (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.

XX PI Van Der Kuyl AC, Cornelissen M;

XX DR WPI; 2002-668396/72.

XX PT Determining presence of a tumor cell or angiogenesis, and the
 PT effectiveness of treatment, by detecting the presence of marker genes
 PT is useful to detect and monitor treatment of Kaposi's Sarcoma
 XX Claim 12; Page 8; 38pp; English.

CC The present invention describes a method for determining if an individual

CC has a tumour cell or site of angiogenesis, or if a treatment is effective
 CC in changing angiogenesis or changing a status of a set of target cells,
 CC comprising determining if a sample of the subject has an expression
 CC product of at least one marker gene. Also described is a compound capable
 CC of altering the expression or activity of Keratin 14, TIE 1, Sialoadhesin
 CC or Siclec in a cell. Peripheral blood mononuclear cell (PBMC)-expressed
 CC Keratin 14, TIE 1, Sialoadhesin or Siclec, and kits containing them from
 CC the present invention can be used in a diagnostic method, particularly as
 CC an indicator of angiogenesis or to determine presence of a tumour cell.
 CC The method of the invention is suitable to determine within a few days if
 CC a certain treatment against Kaposi's Sarcoma is successful. ABQ81851 to
 CC ABQ82006 represent nucleotide sequence used in the exemplification of the
 CC present invention.

XX Sequence 11 BP; 3 A; 4 C; 4 G; 0 U; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1,1e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

11 GGCCAAAGTC 20
 1 GGCCAAAGTC 10

RESULT 138
 ABV62551/c
 ID ABV62551 standard; cDNA; 11 BP.

XX AC ABV62551;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 337.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP15179.

XX PR 03-JAN-2001; 2001DE-1000127.

XX PA (HENK) HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX DR WPI; 2002-590638/63.

XX PT In vitro identification of skin-expressed genes, useful for determining

XX PT homeostasis and identifying cosmetic or pharmaceutical agents against

XX PT e.g. skin cancer

XX PS disclosure; Page 35; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.


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XX Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GGGCCAGGCC 14
DB 10 GGGCCAGGCC 1

RESULT 139
ABV62704
ID ABV62704 standard; cDNA; 11 BP.
AC ABV62704;
XX
XX 21-OCT-2002 (first entry)
DT
XX
DE Human skin EST 490.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antinflammatory; cyostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP15179.
XX
XX 03-JAN-2001; 2001DE-1000127.
XX
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer
XX
XX Disclosure; Page 39; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention.
XX
XX Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GGGCCAGGCC 14
DB 1 GGGCCAGGCC 10

RESULT 140

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```

ABV63037
ID ABV63037 standard; cDNA; 11 BP.
XX
XX AC ABV63037;
XX
XX 21-OCT-2002 (first entry)
DT
XX
DE Human skin EST 823.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antinflammatory; cyostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP15179.
XX
XX 03-JAN-2001; 2001DE-1000127.
XX
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer
XX
XX Disclosure; Page 48; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention.
XX
XX Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 CCAGGCCAAA 17
DB 1 CCGGCCAAA 10

RESULT 141
ABV65097
ID ABV65097 standard; cDNA; 11 BP.
XX
XX AC ABV65097;
XX
XX 21-OCT-2002 (first entry)
DT
XX
DE Human skin EST 2883.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antinflammatory; cyostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX

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OS Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP15179.
XX
XX 03-JAN-2001; 2001DE-1000127.
XX
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
XX Disclosure; Page 105; 1345pp; German.
XX
XX The invention relates to in vitro identification (MI) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (MI) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
XX Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GGGCCGAGGC 13
DB 1 CTGGCCGAGGC 10
RESULT 142
ABV65146
ID ABV65146 standard; cDNA; 11 BP.
XX
XX ABV65146;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human skin EST 2932.
XX
XX Human skin EST 2932.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytosolic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP15179.
XX
XX 03-JAN-2001; 2001DE-1000127.
XX
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX

XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
XX Disclosure; Page 106; 1345pp; German.
XX
XX The invention relates to in vitro identification (MI) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (MI) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
XX Sequence 11 BP; 2 A; 4 C; 5 G; 0 U; 0 other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GGGCCGAGGC 14
DB 2 GAGCCGAGGC 11
RESULT 143
ABV65638/C
ID ABV65638 standard; cDNA; 11 BP.
XX
XX ABV65638;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human skin EST 3424.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytosolic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP15179.
XX
XX 03-JAN-2001; 2001DE-1000127.
XX
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
XX Disclosure; Page 120; 1345pp; German.
XX
XX The invention relates to in vitro identification (MI) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
XX
XX

```
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 other;
XX
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 GGGCAAGTC 20
Db 10 GGGCAAGTC 1

RESULT 144
ABV65978
ID ABV65978 standard; cDNA; 11 BP.
XX
AC ABV65978;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 3764.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytosolic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK ) HENKEL KGAA.
PI Petersohn D, Conradt M, Hofmann K;
XX
WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Disclosure; Page 129; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 other;
XX
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 GGGCAAGTC 20
Db 10 GGGCAAGTC 1

RESULT 145
ABV6142/C
ID ABV6142 standard; cDNA; 11 BP.
XX
AC ABV6142;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 3928.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytosolic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK ) HENKEL KGAA.
PI Petersohn D, Conradt M, Hofmann K;
XX
WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Disclosure; Page 134; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 1 A; 5 C; 3 G; 2 T; 0 other;
XX
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 GGGCAAGTC 20
Db 10 GGGCAAGTC 1

RESULT 146
ABV6964/C
ID ABV6964 standard; cDNA; 11 BP.
XX
AC ABV6964;
XX
```

DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 4750.
 XX
 KW Human, skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP15179.
 XX
 PR 03-JAN-2001; 2001DE-1000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -
 XX
 PS Disclosure; Page 156; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis or
 CC to determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.
 CC
 SQ Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 other;
 XX
 QY Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Db Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 7 GCCAGGCCCA 16
 Db 10 GCCCGGCCCA 1
 XX
 RESULT 147
 ABV67427/c
 ID ABV67427 standard; cDNA; 11 BP.
 XX
 AC ABV67427;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 5213.
 XX
 KW Human, skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200253774-A2.
 XX
 PD 11-JUL-2002.
 XX

XX
 PF 20-DEC-2001; 2001WO-EP15179.
 XX
 PR 03-JAN-2001; 2001DE-1000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -
 XX
 PS Disclosure; Page 169; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.
 CC
 SQ Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 other;
 XX
 QY Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Db Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 5 GCCAGGCC 14
 Db 11 GCCCGGCC 2
 XX
 RESULT 148
 ABV67547
 ID ABV67547 standard; cDNA; 11 BP.
 XX
 AC ABV67547;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 5333.
 XX
 KW Human, skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP15179.
 XX
 PR 03-JAN-2001; 2001DE-1000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against

PT e.g. skin cancer -
XX
PS Disclosure; Page 172; 1345bp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 AGGCCCAAGT 19
DB 2 AGGCCCAAGT 11	
RESULT 149	
ABV68518/c	
ID ABV68518 standard; cDNA; 11 BP.	
XX	
XX ABV68518;	
XX	
DT 21-OCT-2002 (first entry)	
XX	
XX Human skin EST 6304.	
XX	
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;	
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;	
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.	
XX Homo sapiens.	
XX	
XX WO200253774-A2.	
XX	
XX 11-JUL-2002.	
XX	
XX 20-DEC-2001; 2001WO-EP15179.	
XX	
XX 03-JAN-2001; 2001DE-1000127.	
XX	
XX (HENK) HENKEL KGAA.	
XX	
XX Petersohn D, Conradt M, Hofmann K;	
XX WPI; 2002-590638/63.	
XX	
XX In vitro identification of skin-expressed genes, useful for determining	
XX homeostasis and identifying cosmetic or pharmaceutical agents against	
XX e.g. skin cancer -	
XX	
XX Disclosure; Page 200; 1345bp; German.	
XX	
XX The invention relates to in vitro identification (M1) of genes expressed	
XX in the skin of humans or animals by subjecting a mixture of genetically	
XX encoded factors from skin, to serial analysis of gene expression (SAGE)	
XX so as to identify skin-expressed genes and quantify their expression.	
XX (M1) is useful for identifying genes involved in skin homeostasis; to	
XX determine skin homeostasis and to test agent (A) that maintains or	
XX promotes skin homeostasis or that can be used for treating skin	
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;	
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;	
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the	
XX skin. The present sequence is that of a human expressed sequence tag	
XX (EST) of the invention.	
XX	
XX SQ Sequence 11 BP; 1 A; 5 C; 3 G; 2 T; 0 other;	
Query Match 42.0%; Score 8.4; DB 1; Length 11;	
Best Local Similarity 90.0%; Pred. No. 1.1e+02;	
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY 6 GGGCAGGCCA 15	
DB 10 GGGCAGGCCA 1

CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
XX SQ Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TCCGGGCCAG 11
DB 10 TCCGGGCCAG 1	
RESULT 150	
ABV68762/c	
ID ABV68762 standard; cDNA; 11 BP.	
XX	
XX ABV68762;	
XX	
DT 21-OCT-2002 (first entry)	
XX	
XX Human skin EST 6548.	
XX	
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;	
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;	
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.	
XX Homo sapiens.	
XX	
XX WO200253774-A2.	
XX	
XX 11-JUL-2002.	
XX	
XX 20-DEC-2001; 2001WO-EP15179.	
XX	
XX 03-JAN-2001; 2001DE-1000127.	
XX	
XX (HENK) HENKEL KGAA.	
XX	
XX Petersohn D, Conradt M, Hofmann K;	
XX WPI; 2002-590638/63.	
XX	
XX In vitro identification of skin-expressed genes, useful for determining	
XX homeostasis and identifying cosmetic or pharmaceutical agents against	
XX e.g. skin cancer -	
XX	
XX Disclosure; Page 207; 1345bp; German.	
XX	
XX The invention relates to in vitro identification (M1) of genes expressed	
XX in the skin of humans or animals by subjecting a mixture of genetically	
XX encoded factors from skin, to serial analysis of gene expression (SAGE)	
XX so as to identify skin-expressed genes and quantify their expression.	
XX (M1) is useful for identifying genes involved in skin homeostasis; to	
XX determine skin homeostasis and to test agent (A) that maintains or	
XX promotes skin homeostasis or that can be used for treating skin	
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;	
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;	
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the	
XX skin. The present sequence is that of a human expressed sequence tag	
XX (EST) of the invention.	
XX	
XX SQ Sequence 11 BP; 1 A; 5 C; 3 G; 2 T; 0 other;	
Query Match 42.0%; Score 8.4; DB 1; Length 11;	
Best Local Similarity 90.0%; Pred. No. 1.1e+02;	
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY 6 GGGCAGGCCA 15	
DB 10 GGGCAGGCCA 1

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RESULT 151
ABV69053
ID ABV69053 standard; cDNA; 11 BP.
XX
XX ABV69053;
AC
XX 21-OCT-2002 (first entry)
DT
XX Human skin EST 6839.
DE
XX
XX Human; skin; dermatological; vulnery; antiseborrhoeic;
KW immunosuppressive; antineoplastic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
PN
XX 11-JUL-2002.
PD
XX 20-DEC-2001; 2001WO-EP15179.
PF
XX 03-JAN-2001; 2001DE-1000127.
PR
XX (HENKEL ) HENKEL KGAA.
PA
XX (HENKEL ) HENKEL KGAA.
PI Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
DR
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer
XX
XX Disclosure; Page 215; 1345pp; German.
XX
XX The invention relates to in vitro identification (MI) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (MI) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
XX Sequence 11 BP; 3 A; 4 C; 4 G; 0 U; 0 other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 GGCCTAAGTC 20
Dd 1 GGCCTAAGTC 10
RESULT 152
ABV69138/c
ID ABV69138 standard; cDNA; 11 BP.
XX
XX ABV69138;
AC
XX 21-OCT-2002 (first entry)
DT
XX Human skin EST 6924.
DE
XX Human; skin; dermatological; vulnery; antiseborrhoeic;
KW immunosuppressive; antineoplastic; SAGE; neurodermatitis;
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KW immunosuppressive; antineoplastic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
PN
XX 11-JUL-2002.
PD
XX 20-DEC-2001; 2001WO-EP15179.
PF
XX 03-JAN-2001; 2001DE-1000127.
PR
XX (HENKEL ) HENKEL KGAA.
PA
XX (HENKEL ) HENKEL KGAA.
PI Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
DR
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer
XX
XX Disclosure; Page 217; 1345pp; German.
XX
XX The invention relates to in vitro identification (MI) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (MI) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
XX Sequence 11 BP; 0 A; 4 C; 5 G; 2 T; 0 other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCCAGGCCAA 16
Dd 11 GCCAGGCCAA 2
RESULT 153
ABV69411/c
ID ABV69411 standard; cDNA; 11 BP.
XX
XX ABV69411;
AC
XX 21-OCT-2002 (first entry)
DT
XX Human skin EST 7197.
DE
XX Human; skin; dermatological; vulnery; antiseborrhoeic;
KW immunosuppressive; antineoplastic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
PN
XX 11-JUL-2002.
PD
XX 20-DEC-2001; 2001WO-EP15179.
PF
XX 03-JAN-2001; 2001DE-1000127.
PR
XX
```

PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -
 XX
 XX
 PS Disclosure; Page 226; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.
 CC
 SO Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 other;
 XX
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 GCGAGGCCAA 16
 DB 10 GCCAGGCCCA 1
 RESULT 154
 ID ABV69528/c
 ABV69528 standard; cDNA; 11 BP.
 XX
 AC ABV69528;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 7314.
 XX
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KM immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KM psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP15179.
 XX
 PR 03-JAN-2001; 2001DE-1000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -
 XX
 XX Disclosure; Page 229; 1345pp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed

CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.
 CC
 SO Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 other;
 XX
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GGGCCAGGCC 14
 DB 10 GGCCAGTCC 1
 RESULT 155
 ID ABV69972/c
 ABV69972 standard; cDNA; 11 BP.
 XX
 AC ABV69972;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 7758.
 XX
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KM immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KM psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP15179.
 XX
 PR 03-JAN-2001; 2001DE-1000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -
 XX
 XX Claim 24; Page 247; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.
 CC
 SO Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGCC 14
 DB 10 GTGCCAGGCC 1

RESULT 156

ABV70125
 ID ABV70125 standard; cDNA; 11 BP.

AC ABV70125;

DT 21-OCT-2002 (first entry)

DE Human skin EST 7911.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KM psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX Homo sapiens.

PN WO200253774-A2.

PD 11-JUL-2002.

PF 20-DEC-2001; 2001WO-EP15179.

PR 03-JAN-2001; 2001DE-1000127.

XX (HENK) HENKEL KGAA.

PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -

PS Claim 24; Page 252; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.

SO Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGCC 14
 DB 1 GGGCCAGGCC 10

RESULT 157

ABV70458
 ID ABV70458 standard; cDNA; 11 BP.

XX ABV70458;
 AC
 XX 21-OCT-2002 (first entry)

DE Human skin EST 8244.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KM psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX Homo sapiens.

PN WO200253774-A2.

PD 11-JUL-2002.

PF 20-DEC-2001; 2001WO-EP15179.

PR 03-JAN-2001; 2001DE-1000127.

XX (HENK) HENKEL KGAA.

PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -

PS Claim 24; Page 264; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.

SO Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCAGGCCAAA 17
 DB 1 CCGGCCAAA 10

RESULT 158

ABQ86459
 ID ABQ86459 standard; cDNA; 11 BP.

AC ABQ86459;

DT 10-SEP-2002 (first entry)

DE Human skin stress/ageing related EST SEQ ID NO 214.

XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX Homo sapiens.

PN WO200253773-A2.


```

PD 11-JUL-2002.
XX
XX 20-DEC-2001; 2001MO-EP15178.
XX
XX 03-JAN-2001; 2001DE-1000121.
XX
XX (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and ageing; useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential
XX PT gene expression
XX
XX Claim 8; Page 45; 325pp; German.
XX
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (AB086246-AB087680) of the invention.
XX
SQ Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 AGGCCAAGT 19
Db 2 AGGCCCAAGT 11

RESULT 159
AB086573/c
ID AB086573 standard; cDNA; 11 BP.
XX
XX AB086573;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human skin stress/ageing related EST SEQ ID NO 328.
XX
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253773-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001MO-EP15178.
XX
XX 03-JAN-2001; 2001DE-1000121.
XX
XX (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and ageing; useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential
XX PT gene expression
XX

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```

PS Claim 8; Page 50; 325pp; German.
XX
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (AB086246-AB087680) of the invention.
XX
SQ Sequence 11 BP; 0 A; 4 C; 5 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCCAA 16
Db 11 GCCAGGCCCA 2

RESULT 160
AB087161
ID AB087161 standard; cDNA; 11 BP.
XX
XX AB087161;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human skin stress/ageing related EST SEQ ID NO 916.
XX
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253773-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001MO-EP15178.
XX
XX 03-JAN-2001; 2001DE-1000121.
XX
XX (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and ageing; useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential
XX PT gene expression
XX
XX Claim 8; Page 75; 325pp; German.
XX
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (AB086246-AB087680) of the invention.
XX
SQ Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;

```


KM neoangiogenesis; immune response; cytoskeletal; antidiabetic;
 KM ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
 OS Homo sapiens.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US08253.
 XX
 XX 11-APR-2001; 2001US-282850P.
 PR 06-FEB-2002; 2002US-354262P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 PI Garson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 DR WPI; 2003-093016/08.
 XX
 PT New purified human transmembrane protein, designated as tumour
 PT endothelial marker (TEM) 3, useful for detecting, diagnosing or
 PT treating tumour, polycystic kidney disease, diabetic retinopathy,
 PT rheumatoid arthritis or psoriasis -
 XX
 PS Disclosure; Page 104; 374pp; English.
 XX
 CC The present invention relates to a novel method for the isolation of
 CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting,
 CC diagnosing or treating tumours as well as polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are
 CC also useful for inhibiting neoangiogenesis or tumour angiogenesis,
 CC for inducing an immune response to tumour endothelial cells in a
 CC patient, or for identifying candidate drugs for treating tumours.
 CC ABX71828-ABX71999 represent DNA tags for human PEM, TEM or NEM
 CC genes.
 CC
 SQ Sequence 11 BP; 4 A; 3 C; 3 G; 1 T; 0 other;
 XX
 QY Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Db Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 AGGCCAAGT 19
 Db 1 AGGCCAAGT 10
 RESULT 164
 AAA80792
 ID AAA80792 standard; DNA; 8 BP.
 XX
 AC AAA80792;
 DT 24-NOV-2000 (first entry)
 XX
 DE A. thaliana primer walking octamer SEQ ID NO: 105.
 XX
 KM Primer walking; octamer; primer; DNA sequencing; PCR; ss.
 XX
 OS Arabidopsis thaliana.
 PN US6083695-A.
 PD 04-JUL-2000.
 XX
 PF 21-MAY-1997; 97US-0859954.
 PR 15-APR-1996; 96US-0632782.
 XX

XX
 PA (UYHO-) UNIV HOUSTON.
 PA (HARD/) HARDIN S H.
 XX
 PI Hardin PE, Hardin SH, Homayouni R;
 DR WPI; 2000-474852/41.
 XX
 PT Sequencing an unknown DNA molecule for the polymerase chain reaction
 PT and other primer processes comprises primer walking of octamer
 PT oligonucleotides -
 XX
 PS Example 8; Column 77-78; 161pp; English.
 XX
 CC This invention describes a novel method for sequencing an unknown DNA
 CC molecule which comprises selecting a library primer from an octamer
 CC oligonucleotide library consisting of 48 8-bp sequences and
 CC corresponding complementary sequences, where the library primer is
 CC complementary to a known sequence adjacent to the unknown sequence or
 CC is complementary to a sequence in a known extension product. The method
 CC is useful for DNA nucleotide sequencing, in PCR, and in other processes
 CC which make use of primers. The octamers are used to identify coding
 CC sequences. Primer walking using the octamer libraries is advantageous
 CC over other sequencing methods because it does not require multiple
 CC cloning steps nor subsequent template preparations, and it is a
 CC directed and methodical approach. AAA80688-AA81253 represent the octamer
 CC primers used in the primer walking method of the invention.
 CC
 SQ Sequence 8 BP; 3 A; 2 C; 2 G; 1 T; 0 other;
 XX
 QY Query Match 40.0%; Score 8; DB 1; Length 8;
 Db Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 GCCCAAGT 19
 Db 1 GCCCAAGT 8
 RESULT 165
 AAV63091/c
 ID AAV63091 standard; cDNA; 9 BP.
 XX
 AC AAV63091;
 DT 25-JAN-1999 (first entry)
 XX
 DE Human Tcf mutant DNA motif.
 XX
 KM Tcf; beta-catenin; human; drug; familial adenomatous polyposis; FAP;
 KM cancer; adenomatous polyposis coli; APC; neoplastic; ss.
 XX
 OS Homo sapiens.
 PN WO9841631-A2.
 PD 24-SEP-1998.
 XX
 PF 20-MAR-1998; 98WO-US05506.
 XX
 PR 20-MAR-1997; 97US-0821355.
 XX
 PA (UYUT-) RIJKSUNIV UTRECHT.
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Barker N, Clevers H, Kinzler KW, Korinek V, Morin PJ;
 PI Sparks AB, Vogelstein B;
 DR WPI; 1998-531569/45.
 XX
 PT Intronic-free DNA encoding Tcf-4 protein - useful for, e.g.
 PT identifying drugs for treating FAP patients, or patients with
 PT increased risk of developing cancer

XX Example 2; Page 14; 58bp; English.
XX
CC This sequence is a mutant DNA motif from the human Tcf gene family used
CC in the isolation of novel Tcf proteins. These proteins can be used, along
CC with beta-catenin in a method of identifying candidate drugs for use
CC in familial adenomatous polyposis (FAP) patients, or patients with
CC increased risk of developing cancer. The protein can also be used to
CC determine the presence or absence in a cell of wild type adenomatous
CC polyposis coli (APC) gene or a downstream protein in the APC
CC transcription regulatory pathway. This method involves introducing a
CC Tcf-responsive reporter gene into the cell, and measuring transcription
CC of the reporter gene where a cell which supports active transcription of
CC the reporter gene does not have wild type APC or a downstream protein of
CC the APC transcription regulatory pathway. The protein can also be used
CC in a method of diagnosing cancer in a sample suspected of being
CC neoplastic and for treating a patient with colorectal cancer or other
CC cancer associated with FAP, comprising administering to the patient a
CC polypeptide comprising a portion of the APC sequence, comprising the
CC beta-catenin binding site.
XX
SQ Sequence 9 BP; 0 A; 4 C; 2 G; 3 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 11 GGCCCAAG 18
Db 9 GGCCCAAG 2
XX
RESULT 166
AA939683/C
ID AA939683 standard; DNA; 9 BP.
XX
AC AA939683;
XX
DT 05-OCT-1999 (first entry)
XX
DE Tcf optimal response element mutated sequence.
XX
XX Mammalian; transcription factor; Tcf-3; Tcf-4; beta-catenin; mouse;
KM binding domain; Wnt signalling; Wnt/Wingless cascade; anticancer drug;
KM transactivation; fetal cancer; testis cancer; ovary teratoma; mammary;
KM myeloblastoma; medulloblastoma; intestinal cancer; response element; ss.
XX
XX Synthetic.
XX OS
PN EP939122-A1.
XX
XX 01-SEP-1999.
XX
XX 27-FEB-1998; 98EP-0200621.
XX
XX 27-FEB-1998; 98EP-0200621.
XX
XX 27-FEB-1998; 98EP-0200621.
XX
XX (UYUT-) RIJUSUNIV UTRCHT.
XX
XX WPI; 1999-471050/40.
XX
XX New mouse transcription factors, useful for diagnosing and treating
PT cancers and screening for anticancer drugs
PT
XX
XX Disclousure; Page 4; 56bp; English.
XX
XX The invention relates to mammalian transcription factors Tcf-3 or Tcf-4
CC protein or their derivatives. The Tcf proteins of the invention comprise
CC a beta-catenin binding domain and are capable of complexing with beta-
CC catenin in response to signaling through the Wnt/Wingless cascade. The
CC Tcf-3 and Tcf-4 genes, proteins and antibodies against the proteins may
CC be used to screen for candidate anticancer drugs by identifying compounds
CC which interact with beta-catenin/Tcf-3 or beta-catenin/Tcf-4 complexes

CC and alter their transactivation activity. Compounds which interact with
CC the Tcf-3 and Tcf-4 proteins and interfere with their transcriptional
CC activation, identified using these screens, may be used to treat fetal
CC cancer, cancers with stem cell phenotypes, testis or ovary teratomas,
CC myeloblastomas, medulloblastomas, mammary or intestinal cancers. The
CC present sequence represents a mutated Tcf optimal response element
CC motif sequence. Mutation of the element abrogates responsiveness.
XX
SQ Sequence 9 BP; 0 A; 4 C; 2 G; 3 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 11 GGCCCAAG 18
Db 9 GGCCCAAG 2
XX
RESULT 167
ABQ72076/C
ID ABQ72076 standard; DNA; 9 BP.
XX
AC ABQ72076;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2374.
XX
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX WO200242459-A2.
XX
XX 30-MAY-2002.
XX
XX 20-NOV-2001; 2001WO-US43438.
XX
XX 20-NOV-2000; 2000US-0716637.
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX Liu Q;
XX
XX WPI; 2002-500284/53.
XX
XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
XX Example 1; Page 61; 81bp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target sub-site, selecting the F2 zinc finger such
CC that it binds to the S2 target sub-site, and selecting the F3 zinc
CC finger such that it binds to the S3 target sub-site, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplex
CC target sub-sites having the nucleotide G in the 5'-most position of the
CC sub-site. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determine the
CC phenotype and function of gene expression. (I) has improved affinity

CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.

XX Sequence 9 BP; 0 A; 3 C; 4 G; 2 T; 0 other;

SO Query Match 40.0%; Score 8; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CCAGGCCA 15

DB 9 CCAGGCCA 2

RESULT 168

ABQ72078/c

ID ABQ72078 standard; DNA; 9 BP.

XX ABQ72078;

DT 28-AUG-2002 (first entry)

XX Zinc finger protein related oligonucleotide target SEQ ID NO:2376.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX Homo sapiens.

XX Synthetic.

XX MO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US43438.

XX 20-NOV-2000; 2000US-0716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying

XX gene function and for human therapeutics and plant engineering,

XX comprises first, second and third zinc fingers, ordered from N- to

XX C-terminus -

XX Example 1; Page 61; 81bp; English.

XX The present invention describes a zinc finger protein (I) that binds to

XX a target site, comprising a first (F1), a second (F2), and a third (F3)

XX zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the

XX target site comprises, in 3'-5' direction, a first (S1), a second (S2),

XX and a third (S3) target sub-site. Also described are: (1) a polypeptide

XX (II) comprising (1); (2) a polynucleotide (III) encoding (I) or (II); and

XX (3) designing (M) (I) involves selecting the F1 zinc finger such that

XX it binds to the S1 target sub-site, selecting the F2 zinc finger such

XX that it binds to the S2 target sub-site, and selecting the F3 zinc

XX finger such that it binds to the S3 target sub-site, thus designing (I)

XX that binds to a target site. (I) is useful for recognition of triplet

XX target sub-sites having the nucleotide G in the 5'-most position of the

XX sub-site. (I) is useful in studying gene function, and for human

XX therapeutic and plant engineering. (I), (II) or (III) is useful in

XX a subject, in diagnostic methods for sequence specific detection of

XX a target nucleic acid in a sample, and in assays to determine the

XX phenotypic and function of gene expression. (I) has improved affinity

XX and specificity for their target sequences, as well as enhanced

XX biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230

XX represent DNA target sequences and zinc finger peptides which are given

CC in the exemplification of the present invention.

XX Sequence 9 BP; 0 A; 3 C; 4 G; 2 T; 0 other;

SO Query Match 40.0%; Score 8; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CCAGGCCA 15

DB 9 CCAGGCCA 2

RESULT 169

ABQ72126/c

ID ABQ72126 standard; DNA; 9 BP.

XX ABQ72126;

DT 28-AUG-2002 (first entry)

XX Zinc finger protein related oligonucleotide target SEQ ID NO:2424.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX Homo sapiens.

XX Synthetic.

XX MO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US43438.

XX 20-NOV-2000; 2000US-0716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying

XX gene function and for human therapeutics and plant engineering,

XX comprises first, second and third zinc fingers, ordered from N- to

XX C-terminus -

XX Example 1; Page 62; 81bp; English.

XX The present invention describes a zinc finger protein (I) that binds to

XX a target site, comprising a first (F1), a second (F2), and a third (F3)

XX zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the

XX target site comprises, in 3'-5' direction, a first (S1), a second (S2),

XX and a third (S3) target sub-site. Also described are: (1) a polypeptide

XX (II) comprising (1); (2) a polynucleotide (III) encoding (I) or (II); and

XX (3) designing (M) (I) involves selecting the F1 zinc finger such that

XX it binds to the S1 target sub-site, selecting the F2 zinc finger such

XX that it binds to the S2 target sub-site, and selecting the F3 zinc

XX finger such that it binds to the S3 target sub-site, thus designing (I)

XX that binds to a target site. (I) is useful for recognition of triplet

XX target sub-sites having the nucleotide G in the 5'-most position of the

XX sub-site. (I) is useful in studying gene function, and for human

XX therapeutic and plant engineering. (I), (II) or (III) is useful in

XX a subject, in diagnostic methods for sequence specific detection of

XX a target nucleic acid in a sample, and in assays to determine the

XX phenotypic and function of gene expression. (I) has improved affinity

XX and specificity for their target sequences, as well as enhanced

XX biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230

XX represent DNA target sequences and zinc finger peptides which are given

XX in the exemplification of the present invention.

XX Sequence 9 BP; 0 A; 3 C; 4 G; 2 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCA 15
 |||||
 9 CCAGGCCA 2

RESULT 170

AAC73935 AAC73935 standard; cDNA; 10 BP.

XX AAC73935;

DT 02-FEB-2001 (first entry)

DE Human dendritic cell cDNA base sequence oligonucleotide #22.

KM Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 autoimmune disease; tumour; ss.

XX Homo sapiens.

PN WO200060074-A1.

XX 12-OCT-2000.

PF 30-MAR-2000; 2000WO-JP02019.

PR 01-APR-1999; 99JP-0095481.

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PI Hashimoto S, Matsushima K, Suzuki T;

DR WPI; 2000-619172/59.

PT Groups of genes expressed in human dendritic cells at a greater or
 lesser extent than in monocytes for investigation and diagnosis of
 autoimmune disease and tumors

PS Claim 1; Page 9; 95pp; Japanese.

CC The present invention describes a group of genes consisting of 100 genes
 CC which are highly expressed in human dendritic cells; a group of genes
 CC which are expressed at a higher frequency in human dendritic cells than
 CC in human monocytes; and a group of genes which are expressed at lower
 CC frequency in human dendritic cells than in human monocytes. Each group
 CC of genes are characterised in that cDNAs of these genes respectively
 CC have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013),
 CC SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300
 CC (AAC74114 to AAC74213), each is continuous with the base sequence
 CC 5'-CATG-3' located most closely to the poly-A region. The sequences can
 CC be used for the investigation of the role and mechanism of the
 CC involvement of dendritic cells in the immune system and for the study and
 CC diagnosis of diseases in which dendritic cells play a significant role,
 CC e.g. cancers and autoimmune diseases.

XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGC 13
 |||||
 3 GGCCAGGC 10

RESULT 171

ABA06204

ID ABA06204 standard; cDNA; 10 BP.

XX ABA06204;

DT 10-JAN-2002 (first entry)

DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 181.

KM Human; hepatocyte; gene expression; hepatopathy; ss.

XX Homo sapiens.

PN JP2001211883-A.

PD 07-AUG-2001.

PF 31-JAN-2000; 2000JP-0023170.

PR 31-JAN-2000; 2000JP-0023170.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

DR WPI; 2001-629566/73.

PT Human normal hepatocyte expression gene group

PS Claim 1; Page 9; 26pp; Japanese.

CC The invention relates to a human normal hepatocyte expression gene
 CC group comprising 200 genes in the human normal hepatocyte. The
 CC cDNA of each gene comprises one of 200 fully defined nucleotide
 CC sequences as given in the specification. The gene group and the cDNAs
 CC corresponding to each of the genes in the group are useful in the
 CC diagnosis and treatment of human hepatopathy. The present sequence
 CC is a cDNA corresponding to a gene expressed by normal human
 CC hepatocytes.

XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGC 13
 |||||
 3 GGCCAGGC 10

RESULT 172

ID AAH64388 standard; cDNA; 10 BP.

XX AAH64388;

DT 20-SEP-2001 (first entry)

DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1228.

KM Human; transcriptome; gene expression pattern; cancer; drug screening;
 cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

PN WO200138577-A2.

PD 31-MAY-2001.

PF 21-NOV-2000; 2000WO-US31922.

PR 24-NOV-1999; 99US-0448480.

PA (UYJO) UNITV JOHNS HOPKINS.

PI Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 67; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 GGCCAGGC 13
DB 3 GGCCAGGC 10
XX
RESULT 173
AAH64389
ID AAH64389 standard; cDNA; 10 BP.
XX
XX AAH64389;
AC
XX
XX 20-SEP-2001 (first entry)
DT
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1229.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
KM
XX Homo sapiens.
OS
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000MO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PA
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI WPI; 2001-367706/38.
XX
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 67; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX

XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 GGCCAGGC 13
DB 3 GGCCAGGC 10
XX
RESULT 174
AAH64390
ID AAH64390 standard; cDNA; 10 BP.
XX
XX AAH64390;
AC
XX
XX 20-SEP-2001 (first entry)
DT
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1230.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
KM
XX Homo sapiens.
OS
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000MO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PA
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI WPI; 2001-367706/38.
XX
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 67; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 GGCCAGGC 13
DB 3 GGCCAGGC 10
XX
RESULT 175
AAH64391
ID AAH64391 standard; cDNA; 10 BP.
XX
XX AAH64391;
AC
XX

DT 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1231.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000WO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PA
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
DR
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 67; 94pp; English.
PS
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 6 GGGCAGGC 13
DB 3 GGGCAGGC 10
XX
RESULT 176
AAH64392
ID AAH64392 standard; cDNA; 10 BP.
XX
AC AAH64392;
XX
XX 20-SEP-2001 (first entry)
DT
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1232.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000WO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PA

XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
DR
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 67; 94pp; English.
PS
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 6 GGGCAGGC 13
DB 3 GGGCAGGC 10
XX
RESULT 177
AAH64393
ID AAH64393 standard; cDNA; 10 BP.
XX
AC AAH64393;
XX
XX 20-SEP-2001 (first entry)
DT
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1233.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000WO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PA
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
DR
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 67; 94pp; English.
PS
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of

CC the transcriptomes described in the exemplification of the invention.
XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
SQ

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCAGGC 13
DB 3 GGGCAGGC 10

RESULT 178
AAH64394
ID AAH64394 standard; cDNA; 10 BP.
XX
AC AAH64394;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1234.
XX
KM Human; transcriptome; gene expression pattern; cancer; drug screening;
KM cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US31922.
XX
PR 24-NOV-1999; 99US-0448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VB, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
DX
PT New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
PS
XX
XX Claim 13; Page 67; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
XX

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCAGGC 13
DB 3 GGGCAGGC 10

RESULT 179
ABV84947
ID ABV84947 standard; cDNA; 10 BP.
XX
AC ABV84947;

XX
DT 12-DEC-2002 (first entry)
XX
DE Human multiple HCC highly expressed genes SAGE tag #757.
XX
KM SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KM CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KM expression pattern; ss.
XX
OS Homo sapiens.
XX
PN JP2002209591-A.
XX
PD 30-JUL-2002.
XX
PF 19-JAN-2001; 2001JP-0012328.
XX
PR 19-JAN-2001; 2001JP-0012328.
XX
PA (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-631294/68.
XX
PT Human chronic hepatitis C tissue expression exasperating gene group
PT comprises 100 high-ranking genes -
XX
PS
XX
XX Claim 64; Page 31; 139pp; Japanese.
XX
CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the
CC pattern of gene expression in particular cell types. The invention also
CC relates to proteins encoded by the genes expressed in chronic hepatitis
CC C liver tissue or HCC, antibodies against these proteins, and inhibitors
CC of the expression of groups of genes that are overexpressed in chronic
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC treatment of these diseases. Such genes, inhibitors of their expression
CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
CC expressed in hepatocellular carcinoma.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
XX

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCAGGC 13
DB 3 GGGCAGGC 10

RESULT 180
ABV78373
ID ABV78373 standard; cDNA; 10 BP.
XX
AC ABV78373;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human Th2 cell SAGE tag, SEQ ID NO:84.
XX
KM SAGE tag; serial analysis of gene expression; human; Th2 cell;
KM activated T cell; T lymphocyte; immune response; expression pattern;
KM immune disorder; ss.
XX

OS Homo sapiens.
XX
XX JP2002186482-A.
XX
XX 02-JUL-2002.
XX
XX 19-DEC-2000; 2000JP-0385816.
XX
XX 19-DEC-2000; 2000JP-0385816.
XX
XX (KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2002-594261/64.
XX
XX Human activated Th1 and Th2 cell expression gene group, useful for the
XX diagnosis and treatment of Th1 and Th2-related diseases -
XX
XX Claim 10; Page 9; 60pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are expressed in activated human Th1
XX and/or Th2 cells. The SAGE tags of this invention consist of a sequence
XX of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
XX lying nearest to the POLYA region of cDNAs derived from a variety of
XX genes. These tags serve to uniquely identify each transcript and can thus
XX be used to analyse the pattern of gene expression in particular cell
XX types. The invention also relates to proteins encoded by the genes
XX expressed in Th1 and/or Th2 cells, antibodies against these proteins,
XX and inhibitors of the expression of groups of genes that are expressed
XX in either or both the two cell types. Groups of genes expressed in Th1
XX and/or Th2 cell types may be used for the diagnosis and treatment of Th1
XX and Th2-related disorders. Sequences ABV78340-ABV78389 are SAGE tags
XX representing 50 genes which are most highly expressed in Th2 cells.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 GGCCAGGC 13
DB 3 GGCCAGGC 10
XX
RESULT 181
ABL42671
ID ABL42671 standard; cDNA; 10 BP.
XX
XX ABL42671;
XX
XX 12-APR-2002 (first entry)
XX
XX Human maturation/activation dendritic cell expression gene tag #45.
XX
XX Human; maturation/activation dendritic cell expression gene; tag;
XX maturation; activation; dendritic cell; ss.
XX
XX Homo sapiens.
XX
XX JP2001327293-A.
XX
XX 27-NOV-2001.
XX
XX 22-MAY-2000; 2000JP-0150562.
XX
XX 22-MAY-2000; 2000JP-0150562.
XX
XX (KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2002-127070/17.
XX
XX Human maturation/activation dendritic cell expression gene group -
XX

XX
XX Claim 1; Page 9; 41pp; Japanese.
XX
XX The present invention describes a human maturation/activation dendritic
XX cell (DC) expression gene group consisting of 100 genes which show the
XX highest expression among the genes expressed in human maturation/
XX activation DC. Also described are: (1) a protein expressed by the above
XX human maturation/activation DC expression gene; (2) an antibody against
XX the protein; and (3) an antagonist against the expression of each gene
XX belonging to the above gene group. The gene group is useful for the
XX treatment and the diagnosis of various human diseases related to human
XX DC. ABL42672 to ABL42926 represent specifically claimed human
XX maturation/activation DC expression gene tags from the present invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 GGCCAGGC 13
DB 3 GGCCAGGC 10
XX
RESULT 182
AAQ51821/c
ID AAQ51821 standard; RNA; 10 BP.
XX
XX AAQ51821;
XX
XX 25-MAR-2003 (updated)
XX 25-MAY-1994 (first entry)
XX
DE mdr-1 mRNA ribozyme cleavable nucleotide NT585.
XX
XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
XX resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
XX actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
XX adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
XX human; chronic myelogenous leukemia; CML; follicular lymphoma;
XX B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
XX neuroblastoma; lung cancer; genetic drift; mutation; ss.
XX
XX Homo sapiens.
XX
XX WO9323057-A1.
XX
XX 25-NOV-1993.
XX
XX 13-MAY-1993; 93MO-US04573.
XX
XX 14-MAY-1992; 92US-0882822.
XX 14-MAY-1992; 92US-0882885.
XX 26-AUG-1992; 92US-0936110.
XX 26-AUG-1992; 92US-0936421.
XX 26-AUG-1992; 92US-0936422.
XX 26-AUG-1992; 92US-0936531.
XX 26-AUG-1992; 92US-0936532.
XX 07-DEC-1992; 92US-0987131.
XX 19-JAN-1993; 93US-0006122.
XX 19-JAN-1993; 93US-0008910.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Draper KG, Thompson JD;
XX
XX WPI; 1993-386203/48.
XX
XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA
XX associated with tumours or mRNA expressed from gene encoding
XX multiple drug resistance
XX

PS Claim 3; Fig 2; 69pp; English.

XX The sequences given in AA051816-24 represent areas of the multiple

CC drug resistance (mdr-1) mRNA which are accessible to the ribozyme of

CC the invention. The mdr-1 gene encodes a 170 kD integral membrane

CC protein which confers resistance to certain chemotherapeutic agents,

CC such as colchicine, doxorubicin, actinomycin D and vinblastine. The

CC gene is normally expressed in cells of the colon, small intestine,

CC kidney, liver and adrenal gland. High levels of MDR1 transcript

CC have been found in adenocarcinomas that are intrinsically resistant

CC to a broad range of chemotherapeutic agents, such as those derived

CC from adrenal, kidney, liver and bowel. The ribozymes of a transformed

CC may be used to inhibit the development or expression of a transformed

CC phenotype in man and other animals by modulating expression of a gene

CC that contributes to, or inhibits the expression of chronic myelogenous

CC leukemia (CML), promyelocytic leukemia, follicular lymphoma, B-cell

CC neuroblastoma, lung cancer, and other neoplastic conditions.

CC cleavage of target mRNAs expressed in pre-neoplastic and transformed

CC cells elicits inhibition of the transformed state. mdr-1 specific

CC ribozymes remove the mechanism of drug resistance used by transformed

CC cells and thus enhances drug therapies for tumours. The ribozymes may

CC also be used to study genetic drift and mutations within cells.

CC (Updated on 25-MAR-2003 to correct PN field.)

CC

SO Sequence 10 BP; 2 A; 2 C; 3 G; 3 U; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GCCAACT 19

Db 10 GCCAACT 3

RESULT 183

AA096792

ID AA096792 standard; DNA; 10 BP.

XX

AC AA096792;

XX

DT 26-MAR-1996 (first entry)

XX

DE HIV-1 NU4-3 nef gene nucleotide deletion 387.

XX

KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.

XX

OS Human immunodeficiency virus type 1.

XX

PN WO9521912-A1.

XX

PD 17-AUG-1995.

XX

PF 14-FEB-1995; 95MO-AU00063.

XX

PR 23-DEC-1994; 94AU-0000284.

XX

PR 14-FEB-1994; 94AU-0003864.

XX

PR 21-FEB-1994; 94AU-0004002.

XX

PA (AURE-) AUSTRALIAN RED CROSS SOC NSW DIV.

XX

PA (MACF-) MACFARLANE BURNET CENT MEDICAL.

XX

PI Cooper D, Crowe S, Deacon NJ, Learmont JC, McPhee DA;

XX

DR WPI; 1995-293115/38.

XX

XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene

PT or LTR region - can be used in a vaccine to inhibit/reduce

PT productive infection in an individual by a pathogenic strain

XX

PS Claim 13; Page 193; 301pp; English.

CC Attenuation of pathogenic HIV-1 strain NU4-3 involves deletion of 1

CC or more deca-nucleotides (AA096406-097018) from the nef gene and/or

CC 1 or more deca-nucleotides (AA097019-097166) from the LTR region; the

CC sequence of AA096406 corresponds to nucleotides 1-10 of the nef gene

CC (AA096141). The resulting avirulent HIV strains are still capable of

CC inducing an immune response in humans, and enable the generation of

CC therapeutic, diagnostic and targeting agents against HIV-1 infection.

XX

SO Sequence 10 BP; 2 A; 2 C; 6 G; 0 U; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCCAGG 12

Db 2 GGGCCAGG 9

RESULT 184

AA096793

ID AA096793 standard; DNA; 10 BP.

XX

AC AA096793;

XX

DT 26-MAR-1996 (first entry)

XX

DE HIV-1 NU4-3 nef gene nucleotide deletion 388.

XX

KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.

XX

OS Human immunodeficiency virus type 1.

XX

PN WO9521912-A1.

XX

PD 17-AUG-1995.

XX

PF 14-FEB-1995; 95MO-AU00063.

XX

PR 23-DEC-1994; 94AU-0000284.

XX

PR 14-FEB-1994; 94AU-0003864.

XX

PR 21-FEB-1994; 94AU-0004002.

XX

PA (AURE-) AUSTRALIAN RED CROSS SOC NSW DIV.

XX

PA (MACF-) MACFARLANE BURNET CENT MEDICAL.

XX

PI Cooper D, Crowe S, Deacon NJ, Learmont JC, McPhee DA;

XX

DR WPI; 1995-293115/38.

XX

XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene

PT or LTR region - can be used in a vaccine to inhibit/reduce

PT productive infection in an individual by a pathogenic strain

XX

PS Claim 13; Page 193; 301pp; English.

XX

CC Attenuation of pathogenic HIV-1 strain NU4-3 involves deletion of 1

CC or more deca-nucleotides (AA096406-097018) from the nef gene and/or

CC 1 or more deca-nucleotides (AA097019-097166) from the LTR region; the

CC sequence of AA096406 corresponds to nucleotides 1-10 of the nef gene

CC (AA096141). The resulting avirulent HIV strains are still capable of

CC inducing an immune response in humans, and enable the generation of

CC therapeutic, diagnostic and targeting agents against HIV-1 infection.

XX

SO Sequence 10 BP; 1 A; 2 C; 7 G; 0 U; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCCAGG 12

Db 1 GGGCCAGG 8

```

RESULT 185
AAQ8580/c
ID AAQ8580 standard; DNA; 10 BP.
XX
AC AAQ8580;
XX
XX 21-DEC-1995 (first entry)
XX
DE Human mitochondrial D-loop region DNA probe 6-9.
XX
XX Tiling strategy: immobilised nucleic acid probe array;
XX mitochondrial DNA; D-loop region; biological chip;
XX hybridisation fingerprint; interrogation position; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 10
XX /*tag= a
XX /note= "3'-end of probe is covalently attached
XX to chip surface"
XX
XX W09511995-A1.
XX
XX 04-MAY-1995.
XX
XX 26-OCT-1994; 94WC-US12305.
XX
XX 02-AUG-1994; 94US-0284064.
XX
XX 26-OCT-1993; 93US-0143312.
XX
XX (AFVY-) AFFYMAX TECHNOLOGIES NV.
XX
XX Chee M, Cronin MT, Fodor SPA, Gingeras TR, Huang XC;
XX Hubbell EA, Lipschutz RJ, Lobban PE, Miyada CG, Morris MS;
XX Shah N, Sheldon EL;
XX WPI; 1995-178887/23.
XX
XX New arrays of oligo:nucleotide probes - used for comparing known
XX sequences with variants for detection of mutation(s) and sequencing.
XX
XX Disclosure; Page 108; 223pp; English.
XX
XX A DNA chip was prepared for analysing sequences contained in a
XX 1.3kb fragment of human mitochondrial DNA from the D-loop region,
XX the most polymorphic region of human mitochondrial DNA. The chip
XX comprised a set of 268 overlapping oligonucleotide probes (see
XX AAQ8421-Q88684) of varying length (9-14 nucleotides) with varying
XX overlaps arranged in a 1cm x 1cm array. Each position in the
XX sequence was represented by at least one probe (usually 2 or more).
XX DNA was amplified from six human donors and then transcribed to
XX give the 1.3kb RNA transcripts which were fragmented and hybridised
XX to the chip. For each individual, a unique hybridisation fingerprint
XX was produced on the chip; all differences could be correlated with
XX differences in the cloned genomic DNA sequence.
XX
XX Sequence 10 BP; 1 A; 4 C; 5 G; 0 U; 0 other;
XX
XX Query Match 40.0%; Score 8; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TCCGGGCGC 9
XX |||||
XX 8 TCCGGGCGC 1
XX
XX Db
XX
XX RESULT 186
XX AAX54584/c
XX ID AAX54584 standard; DNA; 10 BP.

```

```

XX
XX AAX54584;
XX
AC 05-JUL-1999 (first entry)
XX
DE Human beta tryptase antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impeded respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX chronic obstructive pulmonary disease; leukemia; lymphoma;
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX prostate cancer; ss.
XX
XX Synthetic.
XX
XX W09913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US19419.
XX
XX 09-JUN-1998; 98US-0093972.
XX
XX 17-SEP-1997; 97US-0059160.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction
XX
XX Disclosure; Page 45; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AAX52869-X55771)
XX directed against at least 2 mRNAs selected from target genes, coding and
XX non-coding regions of RNAs corresponding to target genes, gene
XX initiation codons, genomic flanking regions, intron-exon borders, the
XX 5'-end, the 3'-end and the junction between coding and non-coding
XX regions and all segments of RNAs encoding proteins associated with one
XX or more diseases, conditions or mixtures. The antisense oligonucleotides
XX may be derived from sequences AAX5272-74. These multiple target
XX oligonucleotides (specifically AAX55180-271) can be used for the
XX antisense treatment of diseases and conditions. Typical diseases and
XX conditions are those associated with impaired respiration and
XX inflammation, including lung diseases, pulmonary vasoconstriction,
XX inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
XX respiration, respiratory distress syndrome, pain, cystic fibrosis,
XX pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
XX obstructive pulmonary disease (COPD), and cancers such as leukemias,
XX lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
XX pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
XX hepatic metastases, as well as all types of cancers which may metastasize
XX or have metastasized to the lungs, including breast and prostate cancer.
XX
XX Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 other;
XX
XX Query Match 40.0%; Score 8; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 CCAGGCCA 15
XX |||||
XX 8 CCAGGCCA 1
XX
XX Db
XX
XX RESULT 187

```

AAx18625/c
ID AAX18625 standard; DNA; 10 BP.
XX
AC AAX18625;
XX
DT 06-MAY-1999 (first entry)
XX
DE p53 serial analysis of gene expression tag #9.
XX
KM p53; serial analysis of gene expression; SAGE tag; cancer; neoplastic;
KM rat embryo fibroblast; REF; tumour suppressor; cell cycle control;
KM tumorigenesis; diagnosis; ss.
XX
OS Synthetic.
OS Rattus sp.
XX
PN WO9901581-A1.
PD 14-JAN-1999.
XX
PF 02-JUL-1998; 98MO-US13903.
XX
PR 02-JUL-1997; 97US-0051573.
XX
PA (GENZ) GENZYME CORP.
XX
PI Beaudry GA, Bertelsen AH, Galella EA, Madden SL;
XX
DR WPI; 1999-106079/09.
XX
PT Diagnosis of cancer in potentially neoplastic samples - by comparing
PT the level of transcription between RNA transcripts in two tissue
PT samples, useful for providing an extensive profile of gene
PT expression in rat embryo fibroblast (REF) cells
XX
XX Example 2; Page 15; 32pp; English.
XX
CC A method has been developed for the diagnosis of cancer in potentially
CC neoplastic samples. The method comprises comparing the level of
CC transcription between RNA transcripts in two tissue samples (which are
CC of the same type), where the first sample is potentially neoplastic, and
CC the second sample is normal human tissue. The first sample is
CC categorized as neoplastic if its level of transcription is lower than
CC that of the second sample. The transcript is selected from Alu, RAS,
CC US snRNA, 16S RNA, EGR-1, ribosomal protein S27, ETS-1, 28S RNA, CCR1,
CC and LMK-2, and it is identified by a tag selected from ribosomal
CC protein L13a, alpha-tubulin (T1) and (T2), thymosin beta-4, and gamma-
CC actin. The present sequence represents a serial analysis of gene
CC expression (SAGE) tag from the present invention. The use of SAGE tags
CC provides an extensive profile of gene expression in rat embryo
CC fibroblast (REF) cells containing the (non)-functional p53 tumour
CC suppressor gene. The discovery of new SAGE tags, which are regulated
CC by p53, enables the diagnosis of genes that are related to cell cycle
CC control and tumorigenesis.
XX
XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
SQ
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
DE Human beta tryptase polynucleotide fragment #1720.
XX
KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.
XX
XX Homo sapiens.
XX
PN WO200062736-A2.
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000MO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX Claim 14; Page 141; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergies
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
XX Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 other;
SQ
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCA 15
DB 8 CCAGGCCA 1

RESULT 189
AAA56555/c
ID AAA56555 standard; DNA; 10 BP.

AAA56555;

AC 07-SEP-2000 (first entry)

DE Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:449.

XX Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KM granulocyte-macrophage colony-stimulating factor; characterisation;
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KM disease onset mechanism; genetic disease; drug development; ss.

XX Homo sapiens.

OS WO200024892-A1.

PN 04-MAY-2000.

PD 28-OCT-1999; 99WO-JP05982.

PF 28-OCT-1998; 98UP-0307532.

PR (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PA Hashimoto S, Matsushima K, Suzuki T;

PI WPI; 2000-350734/30.

PT Genes most frequently expressed in human monocytes and GM-macrophages
PT and M-macrophages studied and with cDNAs characterized, for study of
PT gene specificity, disease onset mechanism, drug development and
PT diagnosis -

PS Claim 43; Page 129; 138pp; Japanese.

XX The present invention describes 100 human genes, which are expressed
CC most frequently in human monocytes. The cDNA of each gene has a
CC sequence fully defined in the specification, and lacking the CATG
CC sequence located adjacent to polyA region. Also described are:
CC (1) an antibody specifically for the protein encoded by any of the
CC genes; (2) oligonucleotides obtained from the cDNA sequences;
CC (3) 380 human genes which are expressed most frequently in human
CC macrophages, differentiated from human monocytes by
CC granulocyte-macrophage colony-stimulating factor. the cDNA of each gene
CC has a fully defined sequence, given in the specification, lacking the
CC base sequence CATG located most closely to the poly A region;
CC (4) an antibody specifically for the protein encoded by any of the
CC genes of (3); and (5) oligonucleotides obtained from the cDNA sequences
CC of (3). The genes and cDNAs, are used for the study of gene specificity
CC and disease onset mechanism e.g. oncogenesis, genetic diseases, drug
CC development and diagnosis. AAA56107 to AAA56586 represent specifically
CC claimed oligonucleotide tag sequences for human genes expressed in
CC monocytes and macrophages.

XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 other;

QY Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CAGGCCAA 16
DB 10 CAGGCCAA 3

RESULT 190
AAA34031/c
ID AAA34031 standard; DNA; 10 BP.

AAA34031;

AC 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:1720.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KM antiallergic; antiasthmatic; cyostatic; analgesic; impaired away;
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS WO200009525-A2.

PN 24-FEB-2000.

PD 03-AUG-1999; 99WO-US17712.

PF 03-AUG-1998; 98US-0095212.

PR (UYEC-) UNIV EAST CAROLINA.

PA Nyce JW;

PI WPI; 2000-205971/18.

PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -

PS Disclosure; Page 478; 1343pp; English.

XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cyostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA3312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32313 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

XX Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 other;

QY Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CCAGGCCA 15
|||||||
Db 8 CCAGGCCA 1

RESULT 191
AAZ77634/c
ID AAZ77634 standard; DNA; 10 BP.

AAZ77634;
10-APR-2000 (first entry)

Human dendritic cell SAGE tag, SEQ ID NO:62.

SAGE tag; serial analysis of gene expression; antigen-presenting cell;
APC; monocyte-derived dendritic cell; differential gene expression;
immunostimulatory cofactor; costimulatory factor; CTL;
cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

Homo sapiens.
MO9965924-A2.
23-DEC-1999.

18-JUN-1999; 99WO-US13800.
19-JUN-1998; 98US-0089833.
19-JUN-1998; 98US-0089844.
19-JUN-1998; 98US-0089853.
19-JUN-1998; 98US-0089878.
19-JUN-1998; 98US-0089991.
19-JUN-1998; 98US-0089992.
19-JUN-1998; 98US-0089993.
19-JUN-1998; 98US-0089994.
19-JUN-1998; 98US-0089997.
19-JUN-1998; 98US-0089999.
19-JUN-1998; 98US-0090000.
19-JUN-1998; 98US-0090035.
19-JUN-1998; 98US-0090036.
19-JUN-1998; 98US-0090039.
19-JUN-1998; 98US-0090040.
19-JUN-1998; 98US-0090041.
19-JUN-1998; 98US-0090042.
19-JUN-1998; 98US-0090043.
19-JUN-1998; 98US-0090044.
19-JUN-1998; 98US-0090045.
19-JUN-1998; 98US-0090047.
19-JUN-1998; 98US-0090048.
19-JUN-1998; 98US-0090072.
19-JUN-1998; 98US-0090076.
19-JUN-1998; 98US-0090077.
19-JUN-1998; 98US-0090078.
19-JUN-1998; 98US-0090079.
19-JUN-1998; 98US-0090080.
08-DEC-1998; 98US-011715.

(GENZ) GENZYME CORP.
(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.

Roberts BL, Shankara S;
WPI; 2000-106077/09.

Isolated polynucleotides differentially expressed in antigen-presenting
cells; useful in gene vaccines against cancer -
Claim 1; Page 65; 130pp; English.

Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene

expression) tags used to identify mRNA transcripts encoding
immunostimulatory cofactor proteins which are preferentially or
differentially expressed in monocyte-derived dendritic cells compared
with monocytes. Some of the transcripts correspond to known genes or
ESTs (expressed sequence tags) which were previously unknown to be
preferentially or differentially expressed in dendritic cells, while
other transcripts correspond to novel genes. Antigen-presenting cell
(APC)-associated costimulatory factors play an important role in the
activation of the cytotoxic immune response, particularly against tumour
cells. Tumour antigen presentation via the MHC (major histocompatibility
complex) and subsequent recognition by T-cell receptors is alone
insufficient to activate a robust cytotoxic immune response that can
lyse the tumour cells. Immunostimulatory cofactors also being required
for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
sequences identified using the SAGE tags have several potential uses.
They may be used in vaccines to induce an immune response, particularly
against a tumour antigen; to modulate the genotype of an APC; to screen
for agents that modulate expression of differentially expressed genes in
an APC; and as hybridisation probes/amplification primers for the
diagnosis, prognosis and monitoring of diseases related to abnormal
expression of these genes. Detection of the dendritic cell
differentially expressed genes, or of their encoded proteins, can be used
to identify cells as belonging to the monocyte lineage. Cells containing
these genes can be used in active immunotherapy (or to stimulate
production of a population of antigen-specific effector cells) and
vectors containing them are used in gene therapy. Co-administration of
tumour antigens and APC-associated costimulatory factors ensures adequate
antigen presentation to endogenous APCs and upregulates the APCs for the
secretion of T cell growth factors and migration to T cell-rich sites,
recruitment of immune effector cells.

Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 CCAGGCCA 16
|||||||
Db 10 CCAGGCCA 3

RESULT 192
AAZ79103/c
ID AAZ79103 standard; DNA; 10 BP.

AAZ79103;
10-APR-2000 (first entry)

Human dendritic cell SAGE tag, SEQ ID NO:1531.

SAGE tag; serial analysis of gene expression; antigen-presenting cell;
APC; monocyte-derived dendritic cell; differential gene expression;
immunostimulatory cofactor; costimulatory factor; CTL;
cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

Homo sapiens.
MO9965924-A2.
23-DEC-1999.

18-JUN-1999; 99WO-US13800.
19-JUN-1998; 98US-0089833.
19-JUN-1998; 98US-0089844.
19-JUN-1998; 98US-0089853.
19-JUN-1998; 98US-0089878.
19-JUN-1998; 98US-0089991.
19-JUN-1998; 98US-0089992.
19-JUN-1998; 98US-0089993.

PR 19-JUN-1998; 98US-0089994.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0089999.
PR 19-JUN-1998; 98US-0090000.
PR 19-JUN-1998; 98US-0090003.
PR 19-JUN-1998; 98US-0090036.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
PR 19-JUN-1998; 98US-0090042.
PR 19-JUN-1998; 98US-0090043.
PR 19-JUN-1998; 98US-0090044.
PR 19-JUN-1998; 98US-0090045.
PR 19-JUN-1998; 98US-0090047.
PR 19-JUN-1998; 98US-0090048.
PR 19-JUN-1998; 98US-0090072.
PR 19-JUN-1998; 98US-0090076.
PR 19-JUN-1998; 98US-0090077.
PR 19-JUN-1998; 98US-0090078.
PR 19-JUN-1998; 98US-0090079.
PR 19-JUN-1998; 98US-0090080.
PR 08-DEC-1998; 98US-0111715.
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer -
XX
PS Claim 1; Page 109; 130pp; English.
XX
XX Sequences AA27573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or
CC ESTs (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can
CC lyse the tumour cells, immunostimulatory cofactors also being required
CC for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell
CC differentially expressed genes, or of their encoded proteins, can be used
CC to identify cells as belonging to the monocyte lineage. Cells containing
CC these genes can be used in active immunotherapy (or to stimulate
CC production of a population of antigen-specific effector cells) and
CC vectors containing them are used in gene therapy. Co-administration of
CC tumour antigens and APC-associated costimulatory factors ensures adequate
CC antigen presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells.
XX
XX Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 other;
SO

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 13 CCAAGTC 20
|||||
Db 8 CCAAGTC 1
RESULT 193
AA279322/c
ID AA279322 standard; DNA; 10 BP.
XX
AC AA279322;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:1750.
XX
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX APC; monocyte-derived dendritic cell; differential gene expression;
XX immunostimulatory cofactor; costimulatory factor; CTL;
XX cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
XX WO965924-A2.
XX
PD 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US13800.
XX
XX 19-JUN-1998; 98US-0089833.
XX 19-JUN-1998; 98US-0089844.
XX 19-JUN-1998; 98US-0089853.
XX 19-JUN-1998; 98US-0089878.
XX 19-JUN-1998; 98US-0089891.
XX 19-JUN-1998; 98US-0089992.
XX 19-JUN-1998; 98US-0089993.
XX 19-JUN-1998; 98US-0089994.
XX 19-JUN-1998; 98US-0089997.
XX 19-JUN-1998; 98US-0089999.
XX 19-JUN-1998; 98US-0090000.
XX 19-JUN-1998; 98US-0090035.
XX 19-JUN-1998; 98US-0090036.
XX 19-JUN-1998; 98US-0090039.
XX 19-JUN-1998; 98US-0090040.
XX 19-JUN-1998; 98US-0090041.
XX 19-JUN-1998; 98US-0090042.
XX 19-JUN-1998; 98US-0090043.
XX 19-JUN-1998; 98US-0090044.
XX 19-JUN-1998; 98US-0090045.
XX 19-JUN-1998; 98US-0090047.
XX 19-JUN-1998; 98US-0090048.
XX 19-JUN-1998; 98US-0090072.
XX 19-JUN-1998; 98US-0090076.
XX 19-JUN-1998; 98US-0090077.
XX 19-JUN-1998; 98US-0090078.
XX 19-JUN-1998; 98US-0090079.
XX 19-JUN-1998; 98US-0090080.
XX 08-DEC-1998; 98US-0111715.
XX
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer -
XX
PS Claim 1; Page 115; 130pp; English.
XX

CC Sequences AA27573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or
CC ESTs (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can
CC lyse the tumour cells, immunostimulatory cofactors also being required
CC for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell
CC differentially expressed genes, or of their encoded proteins, can be used
CC to identify cells as belonging to the monocyte lineage. Cells containing
CC these genes can be used in active immunotherapy (or to stimulate
CC production of a population of antigen-specific effector cells) and
CC vectors containing them are used in gene therapy. Co-administration of
CC tumour antigens and APC-associated costimulatory factors ensures adequate
CC antigen presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells.

CC SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCCAGGCC 14
Db 10 GCCAGGCC 3

RESULT 194

AA281594/C
ID AA281594 standard; DNA; 10 BP.

AC AA281594;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #828.

KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US13647.

PR 19-JUN-1998; 98US-0089853.

PR 19-JUN-1998; 98US-0089997.

PR 19-JUN-1998; 98US-0090039.

PR 19-JUN-1998; 98US-0090040.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
PI Roberts BL, Shankara S;
DR WPI; 2000-106079/09.
XX
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells; useful for diagnosis,
PT prevention and treatment of cancer -
XX
XX
PS Claim 1; Page 80; 21pp; English.

CC AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines, for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.

CC SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGGCCAG 11
Db 8 CCGGCCAG 1

RESULT 195

AA282082
ID AA282082 standard; DNA; 10 BP.

AC AA282082;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #1316.

KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US13647.

PR 19-JUN-1998; 98US-0089853.

PR 19-JUN-1998; 98US-0089997.

PR 19-JUN-1998; 98US-0090039.

PR 19-JUN-1998; 98US-0090040.

```

XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
PI Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 93; 219pp; English.
XX
CC AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnostics is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCCACG 12
Db 3 GGGCCACG 10

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PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
PI Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 121; 219pp; English.
XX
CC AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnostics is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCCACG 12
Db 3 GGGCCACG 10

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PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 127; 219pp; English.
XX
CC AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 GGGCCACG 12
Db 8 GGGCCACG 1
XX
RESULT 198
AA283787/c
ID AA283787 standard; DNA; 10 BP.
XX
AC AA283787;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #3021.
XX
KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KM non-metastatic breast tumour tissue; gene therapy; anticancer;
KM antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13647.
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XX
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic
PT and non-metastatic breast cancer cells, useful for diagnosis,
PT prevention and treatment of cancer -
XX
PS Claim 1; Page 139; 219pp; English.
XX
CC AA280767 to AA283941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC Diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.
XX
SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 other;
XX
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 GGGCCACG 12
Db 10 GGGCCACG 3
XX
RESULT 199
AA283855
ID AA283855 standard; DNA; 10 BP.
XX
AC AA283855;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #3089.
XX
KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KM non-metastatic breast tumour tissue; gene therapy; anticancer;
KM antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
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XX 18-JUN-1999; 99WO-US13647.
XX
XX 19-JUN-1998; 98US-0089853.
XX 19-JUN-1998; 98US-0089997.
XX 19-JUN-1998; 98US-0090039.
XX 19-JUN-1998; 98US-0090040.
XX 19-JUN-1998; 98US-0090041.
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic
XX and non-metastatic breast cancer cells, useful for diagnosis,
XX prevention and treatment of cancer .
XX
XX Claim 1; Page 141; 219pp; English.
XX
XX AA280767 to AA283941 represent tags corresponding to distinct
XX transcripts that are preferentially transcribed in the metastatic breast
XX tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
XX AA283942 to AA286677 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the primary or non-metastatic
XX breast tumour tissue (i.e. are downregulated in metastatic breast tumour
XX cells). These transcripts can be used for diagnosis, prognosis,
XX monitoring and treatment of breast cancer, particularly where metastatic.
XX reactions is by standard immunoassays or hybridisation/amplification
XX potentially useful for treatment of (metastatic) breast cancer, while
XX promoters from the transcripts are used to direct expression, in selected
XX cell types, of e.g. therapeutic genes (also ribozymes or antisense
XX sequences), particularly an antigen-encoding sequence for use in gene or
XX cell-based vaccines. Polypeptides encoded by the transcripts are also
XX useful in vaccines; for diagnosing breast cancer and for raising
XX specific antibodies (Ab). Ab are used to detect the polypeptides or as
XX therapeutic agents. Host cells that produce the polypeptides can be used
XX to expand and isolate populations of educated, antigen-specific immune
XX effector cells, e.g. cytotoxic T lymphocytes, and these used for
XX adoptive immunotherapy.
XX
XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 other;
XX
XX Query Match 40.0%; Score 8; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 1 GTCCGGGC 8
XX |||||
XX 3 GTCCGGGC 10
XX
XX Db
XX
XX RESULT 200
XX AA283864
XX ID AA283864 standard; DNA; 10 BP.
XX
XX AC AA283864;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell upregulated transcript tag #3098.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
```

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XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US13647.
XX
XX 19-JUN-1998; 98US-0089853.
XX 19-JUN-1998; 98US-0089997.
XX 19-JUN-1998; 98US-0090039.
XX 19-JUN-1998; 98US-0090040.
XX 19-JUN-1998; 98US-0090041.
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic
XX and non-metastatic breast cancer cells, useful for diagnosis,
XX prevention and treatment of cancer .
XX
XX Claim 1; Page 141; 219pp; English.
XX
XX AA280767 to AA283941 represent tags corresponding to distinct
XX transcripts that are preferentially transcribed in the metastatic breast
XX tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
XX AA283942 to AA286677 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the primary or non-metastatic
XX breast tumour tissue (i.e. are downregulated in metastatic breast tumour
XX cells). These transcripts can be used for diagnosis, prognosis,
XX monitoring and treatment of breast cancer, particularly where metastatic.
XX reactions is by standard immunoassays or hybridisation/amplification
XX potentially useful for treatment of (metastatic) breast cancer, while
XX promoters from the transcripts are used to direct expression, in selected
XX cell types, of e.g. therapeutic genes (also ribozymes or antisense
XX sequences), particularly an antigen-encoding sequence for use in gene or
XX cell-based vaccines. Polypeptides encoded by the transcripts are also
XX useful in vaccines; for diagnosing breast cancer and for raising
XX specific antibodies (Ab). Ab are used to detect the polypeptides or as
XX therapeutic agents. Host cells that produce the polypeptides can be used
XX to expand and isolate populations of educated, antigen-specific immune
XX effector cells, e.g. cytotoxic T lymphocytes, and these used for
XX adoptive immunotherapy.
XX
XX Sequence 10 BP; 3 A; 5 C; 2 G; 0 U; 0 other;
XX
XX Query Match 40.0%; Score 8; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 9 CAGGCCAA 16
XX |||||
XX 1 CAGGCCAA 8
XX
XX Db
XX
XX RESULT 201
XX AA284284
XX ID AA284284 standard; DNA; 10 BP.
XX
XX AC AA284284;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell downregulated transcript tag #318.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
```

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XX XX MO9965928-A2.
XX PN
XX XX
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US13647.
XX PR 19-JUN-1998; 98US-0089853.
XX PR 19-JUN-1998; 98US-0089997.
XX PR 19-JUN-1998; 98US-0090039.
XX PR 19-JUN-1998; 98US-0090040.
XX PR 19-JUN-1998; 98US-0090041.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX XX
XX PT Isolated polynucleotides differentially expressed between metastatic
XX PT and non-metastatic breast cancer cells, useful for diagnosis,
XX PT prevention and treatment of cancer -
XX PS Claim 1; Page 152; 219pp; English.
XX XX
XX CC AA280767 to AA283941 represent tags corresponding to distinct
XX CC transcripts that are preferentially transcribed in the metastatic breast
XX CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
XX CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the primary or non-metastatic
XX CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
XX CC cells). These transcripts can be used for diagnosis, prognosis,
XX CC monitoring and treatment of breast cancer, particularly where metastatic.
XX CC Diagnosis is by standard immunoassays or hybridisation/amplification
XX CC reactions. Compounds that modulate expression of the transcripts are
XX CC potentially useful for treatment of (metastatic) breast cancer, while
XX CC promoters from the transcripts are used to direct expression, in selected
XX CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
XX CC sequences), particularly an antigen-encoding sequence for use in gene or
XX CC cell-based vaccines. Polypeptides encoded by the transcripts are also
XX CC useful in vaccines; for diagnosing breast cancer and for raising
XX CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
XX CC therapeutic agents. Host cells that produce the polypeptides can be used
XX CC to expand and isolate populations of educated, antigen-specific immune
XX CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
XX CC adoptive immunotherapy.
XX SQ Sequence 10 BP; 1 A; 2 C; 7 G; 0 U; 0 other;

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```

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCCAGC 12
Db 2 GGGCCAGC 9

```

```

RESULT 202
AA285316/C
ID AA285316 standard; DNA; 10 BP.
XX AC AA285316;
XX XX
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #4550.
XX XX
XX KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KM non-metastatic breast tumour tissue; Gene therapy; anticancer;
XX KM antimetastatic; vaccine; diagnosis; ss.

```

```

XX XX Homo sapiens.
XX OS
XX XX MO9965928-A2.
XX PN
XX XX
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US13647.
XX PR 19-JUN-1998; 98US-0089853.
XX PR 19-JUN-1998; 98US-0089997.
XX PR 19-JUN-1998; 98US-0090039.
XX PR 19-JUN-1998; 98US-0090040.
XX PR 19-JUN-1998; 98US-0090041.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX XX
XX PT Isolated polynucleotides differentially expressed between metastatic
XX PT and non-metastatic breast cancer cells, useful for diagnosis,
XX PT prevention and treatment of cancer -
XX PS Claim 1; Page 181; 219pp; English.
XX XX
XX CC AA280767 to AA283941 represent tags corresponding to distinct
XX CC transcripts that are preferentially transcribed in the metastatic breast
XX CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
XX CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the primary or non-metastatic
XX CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
XX CC cells). These transcripts can be used for diagnosis, prognosis,
XX CC monitoring and treatment of breast cancer, particularly where metastatic.
XX CC Diagnosis is by standard immunoassays or hybridisation/amplification
XX CC reactions. Compounds that modulate expression of the transcripts are
XX CC potentially useful for treatment of (metastatic) breast cancer, while
XX CC promoters from the transcripts are used to direct expression, in selected
XX CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
XX CC sequences), particularly an antigen-encoding sequence for use in gene or
XX CC cell-based vaccines. Polypeptides encoded by the transcripts are also
XX CC useful in vaccines; for diagnosing breast cancer and for raising
XX CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
XX CC therapeutic agents. Host cells that produce the polypeptides can be used
XX CC to expand and isolate populations of educated, antigen-specific immune
XX CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
XX CC adoptive immunotherapy.
XX SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

```

```

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCCAGGCC 14
Db 10 GCCAGGCC 3

```

```

RESULT 203
AA285453/C
ID AA285453 standard; DNA; 10 BP.
XX AC AA285453;
XX XX
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #4687.
XX XX
XX KM Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KM

```

KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US13647.
 XX
 PR 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089997.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 PI Roberts BL, Shankara S;
 DR WPI; 2000-106079/09.
 XX
 PT Isolated polynucleotides differentially expressed between metastatic
 PT and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 XX
 PS Claim 1; Page 184; 219pp; English.
 XX
 PS AA280767 to AA283941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis,
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC Diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines; for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 CC
 XX Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 other;
 SQ
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 CCAAGTC 20
 Db 8 CCAAGTC 1
 RESULT 204
 AA285585/c
 ID AA285585 standard; DNA; 10 BP.
 XX
 AC AA285585;
 XX
 DT 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell downregulated transcript tag #4819.

XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US13647.
 XX
 PR 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089997.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 PI Roberts BL, Shankara S;
 DR WPI; 2000-106079/09.
 XX
 PT Isolated polynucleotides differentially expressed between metastatic
 PT and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 XX
 PS Claim 1; Page 187; 219pp; English.
 XX
 PS AA280767 to AA283941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis,
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC Diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines; for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 CC
 XX Sequence 10 BP; 0 A; 5 C; 2 G; 3 T; 0 other;
 SQ
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGGCCAGG 12
 Db 8 GGGCCAGG 1
 RESULT 205
 AA285596/c
 ID AA285596 standard; DNA; 10 BP.
 XX
 AC AA285596;
 XX
 DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell downregulated transcript tag #4830.
 XX XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 XX antineoplastic; vaccine; diagnosis; ss.
 OS Homo sapiens.
 XX MO965928-A2.
 XX PN WO965928-A2.
 XX PD 23-DEC-1999.
 XX PF 18-JUN-1999; 99WO-US13647.
 XX PR 19-JUN-1998; 98US-0089853.
 XX PR 19-JUN-1998; 98US-0089997.
 XX PR 19-JUN-1998; 98US-0090039.
 XX PR 19-JUN-1998; 98US-0090040.
 XX PR 19-JUN-1998; 98US-0090041.
 XX PA (GENZ) GENZYME CORP.
 XX PA (ROBE/) ROBERTS B L.
 XX PA (SHAN/) SHANKARA S.
 XX PI Roberts BL, Shankara S;
 XX DR WPI, 2000-106079/09.
 XX PT Isolated polynucleotides differentially expressed between metastatic
 PT and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 XX Claim 1; Page 188; 219pp; English.
 XX PS
 CC AA280767 to AA283941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis,
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines; for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 CC XX
 XX Sequence 10 BP; 0 A; 6 C; 2 G; 2 T; 0 other;
 SQ
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGGCCAGG 12
 Db 8 GGGCCAGG 1
 RESULT 206
 AA285958 standard; DNA; 10 BP.
 XX
 AC AA285958;

XX DT 07-APR-2000 (first entry)
 XX DE Metastatic breast tumour cell downregulated transcript tag #5192.
 XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 XX antineoplastic; vaccine; diagnosis; ss.
 OS Homo sapiens.
 XX MO965928-A2.
 XX PN WO965928-A2.
 XX PD 23-DEC-1999.
 XX PF 18-JUN-1999; 99WO-US13647.
 XX PR 19-JUN-1998; 98US-0089853.
 XX PR 19-JUN-1998; 98US-0089997.
 XX PR 19-JUN-1998; 98US-0090039.
 XX PR 19-JUN-1998; 98US-0090040.
 XX PR 19-JUN-1998; 98US-0090041.
 XX PA (GENZ) GENZYME CORP.
 XX PA (ROBE/) ROBERTS B L.
 XX PA (SHAN/) SHANKARA S.
 XX PI Roberts BL, Shankara S;
 XX DR WPI, 2000-106079/09.
 XX PT Isolated polynucleotides differentially expressed between metastatic
 PT and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 XX Claim 1; Page 196; 219pp; English.
 XX PS
 CC AA280767 to AA283941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis,
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines; for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 CC XX
 XX Sequence 10 BP; 2 A; 2 C; 6 G; 0 U; 0 other;
 SQ
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGGCCAGG 12
 Db 2 GGGCCAGG 9
 RESULT 207
 ABA06090 standard; cDNA; 10 BP.
 ID ABA06090

XX ABA06090;
AC
XX
XX
DT 10-JAN-2002 (first entry)
XX
DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 67.
XX
XX Human; hepatocyte; gene expression; hepatopathy; ss.
XX
XX Homo sapiens.
XX JP2001211883-A.
XX
XX 07-AUG-2001.
XX
XX 31-JAN-2000; 2000JP-0023170.
XX
XX 31-JAN-2000; 2000JP-0023170.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2001-629566/73.
XX
XX Human normal hepatocyte expression gene group -
XX
XX Claim 1; Page 7; 26pp; Japanese.
XX
XX The invention relates to a human normal hepatocyte expression gene
XX group comprising 200 genes in the human normal hepatocyte. The
XX cDNA of each gene comprises one of 200 fully defined nucleotide
XX sequences as given in the specification. The gene group and the cDNAs
XX corresponding to each of the genes in the group are useful in the
XX diagnosis and treatment of human hepatopathy. The present sequence
XX is a cDNA corresponding to a gene expressed by normal human
XX hepatocytes.
XX
XX Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;
SQ
XX
XX Query Match 40.0%; Score 8; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1,1e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 CAGGCCAA 16
DB 2 CAGGCCAA 9
XX
XX RESULT 208
XX AAH63781
XX ID AAH63781 standard; cDNA; 10 BP.
XX
XX AAH63781;
AC
XX
XX 20-SEP-2001 (first entry)
DT
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 621.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
XX
XX MO200138577-A2.
XX
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US31922.
XX
XX 24-NOV-1999; 99US-0448480.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX

XX WPI; 2001-367706/38.
DR
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX Claim 13; Page 53; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences
XX AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
XX in the invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of
XX the transcriptomes described in the exemplification of the invention.
XX
XX Sequence 10 BP; 1 A; 2 C; 7 G; 0 U; 0 other;
SQ
XX
XX Query Match 40.0%; Score 8; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1,1e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCCAGG 12
DB 1 GGGCCAGG 8
XX
XX RESULT 209
XX AAH64036/c
XX ID AAH64036 standard; cDNA; 10 BP.
XX
XX AAH64036;
AC
XX
XX 20-SEP-2001 (first entry)
DT
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 876.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
XX
XX MO200138577-A2.
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000WO-US31922.
XX
XX 24-NOV-1999; 99US-0448480.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX
XX WPI; 2001-367706/38.
DR
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX Claim 13; Page 59; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences
XX AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
XX in the invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of
XX the transcriptomes described in the exemplification of the invention.
XX


```

SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;
  Query Match 40.0%; Score 8; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred. No. 1.1e+02;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
  OY 7 GCCAGGCC 14
  DB 10 GCCAGGCC 3

RESULT 210
AAH64037/C
ID AAH64037 standard; cDNA; 10 BP.
XX
XX AAH64037;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SRO ID NO: 877.
DE
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US31922.
XX
XX 24-NOV-1999; 99US-0448480.
XX
XX (UJJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX WPI; 2001-367706/38.
XX
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 59; 94pp; English.
XX
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
XX
XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;
SQ
  Query Match 40.0%; Score 8; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred. No. 1.1e+02;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
  OY 7 GCCAGGCC 14
  DB 10 GCCAGGCC 3

RESULT 211
AAH64374/C
ID AAH64374 standard; cDNA; 10 BP.
XX
XX AAH64374;
XX
XX 20-SEP-2001 (first entry)

```

```

XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1214.
XX XX
XX XX Human, transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS
XX XX Homo sapiens.
XX XX
XX PN WO200138577-A2.
XX PD
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US31922.
XX PR 24-NOV-1999; 99US-0448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velulescu VE, Vogelstein B, Kinzler KW;
XX DR WPI; 2001-367706/38.
XX XX
XX XX New isolated polynucleotides, useful for identifying specific cell
XX PT type, such as cancer cell, comprises transcriptomes expressed in
XX PT particular cell types -
XX XX
XX PS Claim 13; Page 67; 94pp; English.
XX XX
XX CC The present invention describes a method of identifying the type of cell
XX CC in a sample, involving determining which of the sequences
XX CC AA63161-AA64724 is expressed by the cell. The transcriptomes described
XX CC in the invention are cell-type specific, cancer specific or ubiquitously
XX CC expressed in humans. They can also be used to screen for drugs, reduce
XX CC cancer specific gene expression, standardise expression and restore the
XX CC function of a diseased cell or tissue. The present sequence is one of
XX CC the transcriptomes described in the exemplification of the invention.
XX XX
XX XX Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;
XX XX
OY Query Match 40.0%; Score 8; DB 1; Length 10;
DB Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
6 GGCCAGGC 13
8 GGCCAGGC 1
XX
RESULT 212
AAH64375/C
XX ID AAH64375 standard; cDNA; 10 BP.
XX AC
XX AC AAH64375;
XX XX
XX DT 20-SEP-2001 (first entry)
XX XX
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1215.
XX XX
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US31922.
XX PR 24-NOV-1999; 99US-0448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI
XX DR
XX XX

```

PI Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-36706/38.
XX
XX
PT New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcripts expressed in
PT particular cell types -
XX
XX
PS Claim 13; Page 67; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcripts described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcripts described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGC 13
DB 8 GGCCAGGC 1

RESULT 213
AAH32825
ID AAH32825 standard; cDNA; 10 BP.
XX
XX AAH32825;
AC
XX 13-AUG-2001 (first entry)
DT
XX
XX LPS activated human monocyte expression gene cDNA tag SEQ.198.
DE
XX
XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KM expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
XX Homo sapiens.
OS
XX JP2001069993-A.
PN
XX 21-MAR-2001.
PD
XX 28-APR-2000; 2000JP-0131079.
PF
XX 08-JUL-1999; 99JP-0195103.
PR
XX (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.
PA
XX WPI; 2001-304369/32.
DR
XX LPS activated human monocyte expression gene group -
PT
XX Claim 19; Page 36; 52pp; Japanese.
PS
XX
XX The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence
CC 5'-CATG-3' nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role.
CC AAH32628 to AAH32943 represent specifically claimed LPS activated human
CC monocyte expression gene cDNA tags from the present invention. AAH32944
CC represents an LPS activated human monocyte expression gene cDNA sequence
CC encoding AAB98009, which are given in the exemplification of the present

CC invention.
XX
XX Sequence 10 BP; 1 A; 2 C; 7 G; 0 U; 0 other;
SQ
XX
XX Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGCCAGGC 12
DB 1 GGCCAGGC 8

RESULT 214
AAH32856/c
ID AAH32856 standard; cDNA; 10 BP.
XX
XX AAH32856;
AC
XX 13-AUG-2001 (first entry)
DT
XX
XX LPS activated human monocyte expression gene cDNA tag SEQ.229.
DE
XX
XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KM expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
XX Homo sapiens.
OS
XX JP2001069993-A.
PN
XX 21-MAR-2001.
PD
XX 28-APR-2000; 2000JP-0131079.
PF
XX 08-JUL-1999; 99JP-0195103.
PR
XX (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.
PA
XX WPI; 2001-304369/32.
DR
XX LPS activated human monocyte expression gene group -
PT
XX Claim 19; Page 39; 52pp; Japanese.
PS
XX
XX The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence
CC 5'-CATG-3' nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role.
CC AAH32628 to AAH32943 represent specifically claimed LPS activated human
CC monocyte expression gene cDNA tags from the present invention. AAH32944
CC represents an LPS activated human monocyte expression gene cDNA sequence
CC encoding AAB98009, which are given in the exemplification of the present
CC invention.
XX
XX Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGC 13
DB 8 GGCCAGGC 1

RESULT 215
AAH39487/c
ID AAH39487 standard; DNA; 10 BP.
XX

AC AAF39487;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6226.
 XX
 KM Yeast; *Saccharomyces cerevisiae*; characterisation; cell cycle; NORF;
 KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KM serial analysis of gene expression; antifungal; tag; identification;
 KM linker; PCR primer; ds.
 XX
 OS *Saccharomyces cerevisiae*.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US16223.
 XX
 PR 16-JUN-1999; 99US-0335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis
 PT of gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle -
 XX
 PS Example; Page 222; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a
 CC yeast cell; and (b) monitoring expression of a NORF gene whose
 CC expression varies as in M1, where a test substance which modifies the
 CC expression of the yeast gene is a candidate antifungal drug; (3) a method
 CC (M3) for identifying human genes which are involved in cell cycle
 CC progression comprising contacting human DNA with a probe which comprises
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
 CC member of a class of drugs having a characteristic effect on gene
 CC expression in a yeast cell comprising contacting a yeast cell with a
 CC candidate drug and monitoring expression in the yeast cell of at least 1
 CC NORF gene whose expression is affected by the class of drugs. The NORF
 CC genes may be used to study, monitor and affect phases of the cell cycle,
 CC the differentially expressed genes may be used as markers of phases of
 CC the cell cycle. The methods may be used to identify candidate drugs which
 CC affect the cell cycle and for identification of antifungal drugs.
 CC AAF3268 to AAF4064 represent SAGE tags used in the exemplification of
 CC the present invention. AAF3262 to AAF3267 represent linkers and PCR
 CC primers used in the SAGE method, in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 216
 ID AAF41493/c
 XX AAF41493 standard; DNA, 10 BP.
 XX
 AC AAF41493;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8232.
 XX
 KM Yeast; *Saccharomyces cerevisiae*; characterisation; cell cycle; NORF;
 KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KM serial analysis of gene expression; antifungal; tag; identification;
 KM linker; PCR primer; ds.
 XX
 OS *Saccharomyces cerevisiae*.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US16223.
 XX
 PR 16-JUN-1999; 99US-0335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis
 PT of gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle -
 XX
 PS Example; Page 294; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a
 CC yeast cell; and (b) monitoring expression of a NORF gene whose
 CC expression varies as in M1, where a test substance which modifies the
 CC expression of the yeast gene is a candidate antifungal drug; (3) a method
 CC (M3) for identifying human genes which are involved in cell cycle
 CC progression comprising contacting human DNA with a probe which comprises
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
 CC member of a class of drugs having a characteristic effect on gene
 CC expression in a yeast cell comprising contacting a yeast cell with a
 CC candidate drug and monitoring expression in the yeast cell of at least 1
 CC NORF gene whose expression is affected by the class of drugs. The NORF
 CC genes may be used to study, monitor and affect phases of the cell cycle,
 CC the differentially expressed genes may be used as markers of phases of
 CC the cell cycle. The methods may be used to identify candidate drugs which
 CC affect the cell cycle and for identification of antifungal drugs.
 CC AAF3268 to AAF4064 represent SAGE tags used in the exemplification of
 CC the present invention. AAF3262 to AAF3267 represent linkers and PCR
 CC primers used in the SAGE method, in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 CAGGCCA 2

RESULT 217

ABV84307 standard; cDNA; 10 BP.

ABV84307;

12-DEC-2002 (first entry)

Human chronic hepatitis C tissue underexpressed EST SAGE tag #117.

SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; EST; expressed sequence tag; ss.

Homo sapiens.

JP2002209591-A.

30-JUL-2002.

19-JAN-2001; 2001JP-0012328.

19-JAN-2001; 2001JP-0012328.

(KAGAKU GIUTSU SHINKO JIGYODAN.

WPI; 2002-631294/68.

Human chronic hepatitis C tissue expression exasperating gene group

comprises 100 high-ranking genes -

Claim 10; Page 13; 139pp; Japanese.

The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C-induced hepatocellular carcinoma (HCC) compared with normal human liver tissue. The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes that are overexpressed in chronic hepatitis C liver tissue or HCC. Groups of genes differentially expressed in chronic hepatitis C tissue or HCC may be used for the diagnosis and treatment of these diseases. Such genes, inhibitors of their expression or activity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences ABV84291-ABV84390 are SAGE tags representing the 100 least highly expressed genes out of those genes which are underexpressed in chronic hepatitis C liver tissue compared with normal liver tissue.

Sequence 10 BP; 5 A; 2 C; 3 G; 0 U; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

10 AGGCCAAA 17

2 AGGCCAAA 9

RESULT 218

ABV84789 standard; cDNA; 10 BP.

ABV84789;

12-DEC-2002 (first entry)

Human gamma-glutamyltransferase 1 SAGE tag #599.

SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; ss.

Homo sapiens.

JP2002209591-A.

30-JUL-2002.

19-JAN-2001; 2001JP-0012328.

19-JAN-2001; 2001JP-0012328.

(KAGAKU GIUTSU SHINKO JIGYODAN.

WPI; 2002-631294/68.

Human chronic hepatitis C tissue expression exasperating gene group

comprises 100 high-ranking genes -

Claim 46; Page 27; 139pp; Japanese.

The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C-induced hepatocellular carcinoma (HCC) compared with normal human liver tissue. The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes that are overexpressed in chronic hepatitis C liver tissue or HCC. Groups of genes differentially expressed in chronic hepatitis C tissue or HCC may be used for the diagnosis and treatment of these diseases. Such genes, inhibitors of their expression or activity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences ABV84691-ABV84790 are SAGE tags representing the 100 least highly expressed genes out of those genes which are underexpressed in hepatocellular carcinoma compared with chronic hepatitis C liver tissue.

Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 GGGCCAGG 12

3 GGGCCAGG 10

RESULT 219

ABV78459 standard; cDNA; 10 BP.

ABV78459;

29-NOV-2002 (first entry)

Human Thi cell preferentially expressed EST SAGE tag, SEQ ID NO:170.

SAGE tag; serial analysis of gene expression; human; Thi cell;

KM activated T cell; T lymphocyte; immune response; expression pattern;
 KM preferential expression; immune disorder; EST; expressed sequence tag;
 SS.
 XX Homo sapiens.
 XX JP2002186482-A.
 XX
 XX
 XX 02-JUL-2002.
 PD
 XX 19-DEC-2000; 2000JP-0385816.
 PF
 XX 19-DEC-2000; 2000JP-0385816.
 PR
 XX (KAGAKU GIUTSU SHINKO JIGYODAN.
 PA WPI; 2002-594261/64.
 DR
 XX
 XX
 PT Human activated Th1 and Th2 cell expression gene group, useful for the
 PT diagnosis and treatment of Th1 and Th2-related diseases -
 XX
 PS Claim 19; Page 11; 60pp; Japanese.
 XX
 CC The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are expressed in activated human Th1
 CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
 CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
 CC lying nearest to the polyA region of cDNAs derived from a variety of
 CC genes. These tags serve to uniquely identify each transcript and can thus
 CC be used to analyse the pattern of gene expression in particular cell
 CC types. The invention also relates to proteins encoded by the genes
 CC expressed in Th1 and/or Th2 cells, antibodies against these proteins,
 CC and inhibitors of the expression of groups of genes that are expressed
 CC in either or both the two cell types. Groups of genes expressed in Th1
 CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
 CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
 CC representing 171 genes which are more highly expressed in Th1 cells
 CC compared with Th2 cells.
 XX
 SQ Sequence 10 BP; 4 A; 2 C; 4 G; 0 U; 0 other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GGCCAAAG 18
 Db 1 GGCCAAAG 8
 RESULT 220
 ABL57664
 ID ABL57664 standard; DNA; 10 BP.
 XX
 XX ABL57664;
 AC
 XX
 XX 08-OCT-2002 (first entry)
 DT
 XX
 XX Human SCYA24 primer-extension oligonucleotide #19.
 DE
 XX
 XX SCYA24; human; small inducible cytokine; isogene; antiasthmatic; asthma;
 KM gene therapy; respiratory inflammatory disease; polymorphism; primer;
 KM primer extension; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200220851-A1.
 PN
 XX
 XX 14-MAR-2002.
 PD
 XX
 XX 10-SEP-2001; 2001WO-US28328.
 PF
 XX
 PR 08-SEP-2000; 2000US-231129P.

XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 XX Anastasio AE, Han J, Kazemi A;
 PI
 XX
 XX WPI; 2002-351785/38.
 DR
 XX
 XX
 PT New genetic variants of small inducible cytokine subfamily A member 24
 PT gene, useful in studying expression and function of the protein, and
 PT for screening drugs to treat diseases such as asthma -
 XX
 PS Claim 18; Page 15; 98pp; English.
 XX
 CC The invention relates to a novel isolated polynucleotide comprising a
 CC small inducible cytokine subfamily A (cys-cys), member 24 (SCYA24)
 CC isogene. The polypeptide of the invention has antiasthmatic activity. The
 CC polynucleotide may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful in the development of drugs for treating
 CC diseases associated with SCYA24 activity, e.g. respiratory inflammatory
 CC diseases such as asthma. The 3' end sequences of oligonucleotide primers
 CC used for detecting polymorphisms in the SCYA24 gene by primer extension
 CC are represented in ABU57646-ABU57675.
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGCCGACG 12
 Db 3 GGCCGACG 10
 RESULT 221
 ABK95840
 ID ABK95840 standard; DNA; 10 BP.
 XX
 XX ABK95840;
 AC
 XX
 XX 24-SEP-2002 (first entry)
 DT
 XX
 XX Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #11.
 DE
 XX
 XX Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
 KM glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
 KM amino acid transporter disorder; single nucleotide polymorphism; SNP.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200244198-A2.
 PN
 XX
 XX 06-JUN-2002.
 PD
 XX
 XX 29-NOV-2001; 2001WO-US44781.
 PF
 XX
 XX 30-NOV-2000; 2000US-250254P.
 PR
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX
 XX Bieganski KM, Kazemi A, Russo DP, Sauser EA;
 PI
 XX
 XX WPI; 2002-519580/55.
 DR
 XX
 XX Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
 PT Amino Acid Transporter), Member 4 isogenes, for improving efficiency
 PT and reliability in drug development for treating cancers -
 XX
 PS Claim 17; Page 16; 139pp; English.
 XX
 XX The invention relates to an isolated polynucleotide (i) comprising a
 CC first nucleotide sequence which comprises solute carrier family 1
 CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes

CC (11) and an isolated polypeptide (111) comprising an amino acid sequence
CC which is a polymorphic variant of a reference sequence for SLCL14
CC protein. Also described are methods for: (1) haplotyping or genotyping
CC SLCL14 gene of an individual; (2) predicting a haplotype pair for SLCL14
CC gene of an individual; (3) identifying an association between a trait and
CC at least one haplotype or haplotype pair of SLCL14 gene. (111) is useful
CC in screening for drugs targeting (111) that are useful for treating
CC cancer, neurological diseases and amino acid transporter disorders. The
CC methods are useful for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with SLCL14 activity. The haplotyping method is also
CC used by the pharmaceutical research scientist to validate SLCL14 as a
CC candidate target for treating a specific condition or disease predicted
CC to be associated with SLCL14 activity, e.g. cancer, neurological diseases
CC and amino acid transporter disorders, and in the design of clinical
CC trials for treating a specific condition of disease associated with
CC SLCL14 activity. The methods are also useful for screening compounds
CC targeting SLCL14. Anti-SLCL14 antibody is useful in diagnostic,
CC prognostic and therapeutic methods. ABR95761-ABR95877 represent
CC SLCL14 gene allele-specific oligonucleotides, primer extension
CC oligonucleotides and related PCR primers used to identify single
CC nucleotide polymorphisms (SNP) of the gene.

CC Sequence 10 BP; 1 A; 6 C; 3 G; 0 U; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCCAGGCC 14
Db 2 GCCAGGCC 9

RESULT 222

ABK72637/C
ID ABK72637 standard; DNA; 10 BP.

AC ABK72637;

XX 30-JUL-2002 (first entry)

XX Leukotriene B4 receptor primer extension oligonucleotide #9.

XX Human; leukotriene B4; receptor; chemokine receptor-like 1; LTB4R;

XX Chemottractant; inflammation; immune response; infection;

KM inflammatory disorder; recombinant non-human animal;

KW primer extension oligonucleotide; ss.

XX Homo sapiens.

XX WO200230949-A2.

XX 18-APR-2002.

XX 12-OCT-2001; 2001WO-US32002.

XX 13-OCT-2000; 2000US-240223P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Bieglecki KM, Chew A, Koshy B, Sanchis A, Sausker EA;

XX WPI; 2002-416857/44.

XX Novel isolated human leukotriene B4 receptor polynucleotide, useful for
XX therapeutic purposes, for studying expression and function of the
XX polynucleotide, and for expressing the receptor -
XX Claim 17; Page 14; 69pp; English.

XX The invention describes an isolated human leukotriene B4 receptor
XX (chemokine receptor-like 1) (LTB4R) polynucleotide (I) comprising a

CC sequence which is a polymorphic variant for a reference sequence for the
CC LTB4R gene or its fragment, or a polymorphic variant of a reference
CC sequence for a LTB4R cDNA or its fragment. LTB4R is a potent
CC chemottractant that is primarily involved in inflammation, immune
CC responses and host defense against infection. (1) is useful in studying
CC the expression and function of LTB4R, and in expressing LTB4R protein for
CC use in screening for candidate drugs to treat diseases related to LTB4R
CC activity, e.g. inflammatory disorders. A recombinant non-human animal is
CC useful for studying expression of the LTB4R isogenes in vivo, for in vivo
CC screening and testing of drugs targeted against LTB4R protein, and for
CC testing the efficacy of therapeutic agents and compounds for diseases
CC associated with LTB4R activity, e.g. inflammatory disorders, in a
CC biological system. This sequence represents a primer extension
CC oligonucleotide used for detecting polymorphisms in the leukotriene
CC B4 receptor (LTB4R) gene.

CC Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGGGCCA 10
Db 10 CCGGGCCA 3

RESULT 223

ABK17015/C
ID ABK17015 standard; DNA; 10 BP.

AC ABK17015;

XX 26-MAR-2002 (first entry)

XX Pyridoxal (pyridoxine, vitamin B6) Kinase (PDXK) primer #8.

XX Pyridoxal kinase; pyridoxine; vitamin B6; PDXK

KM autoimmune polyglandular disease type 1; transgenic animal;

KW gene therapy; primer extension; primer; ss.

XX Homo sapiens.

XX WO200190125-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US16909.

XX 24-MAY-2000; 2000US-206664P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Chew A, Duda A, Koshy B;

XX WPI; 2002-106169/14.

XX Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polynts,
XX useful for therapeutic purposes, for studying the expression and
XX function of the polynucleotide, and for expressing pyridoxal protein -
XX Claim 19; Page 14; 135pp; English.

XX The invention describes an isolated human pyridoxal (pyridoxine, vitamin
XX B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in
XX studying the expression and function of PDXK, and in expressing PDXK
XX protein for use in screening for candidate drugs to treat PDXK related
XX diseases and for therapeutic purposes. A transgenic animal is useful for
XX studying expression of the PDXK isogenes in vivo, for in vivo screening
XX and testing of drugs targeted against PDXK protein, and for testing the
XX efficacy of therapeutic agents and compounds for autoimmune polyglandular
XX disease type 1. The polypeptide is useful for studying the effect of the
XX variation on the biological activity of PDXK and the binding affinity of

CC candidate drugs targeting PDXK for the treatment of autoimmune
 CC polyglutamine disease type 1. Genotyping and haplotyping is useful for
 CC improving the efficacy and reliability of several steps in the discovery
 CC and development of drugs for treating diseases associated with PDXK
 CC activity, e.g., autoimmune polyglutamine disease type 1, to validate PDXK
 CC as a candidate agent for treating a specific condition or disease
 CC predicted to be associated with PDXK activity, and in the design of
 CC clinical trials of candidate drugs. This sequence is one of 38 (see
 CC ABK16978-ABK17015) primers used for detecting PDXK gene polymorphisms
 CC by primer extension techniques, described in the method of the invention.
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CCAGGCCA 15
 Db 9 CCAGGCCA 2
 RESULT 224
 AAS99416
 ID AAS99416 standard; DNA; 10 BP.
 XX
 AC AAS99416;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Aldenhyde dehydrogenase 5 family, member A1, oligonucleotide #109.
 XX
 KW Aldenhyde dehydrogenase 5 family member A1; ALDH5A1;
 KW succinate-semialdehyde dehydrogenase; gene therapy; primer;
 KW antisense technology; primer extension oligonucleotide;
 KW 4-hydroxybutyric aciduria; metabolic disease; transgenic animal;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN WO200190119-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 21-MAY-2001; 2001WO-US16558.
 XX
 PR 19-MAY-2000; 2000US-205849P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Kiem SE, Koshy B, Tanguay DA;
 XX
 DR WPI; 2002-089912/12.
 XX
 PT New genetic variants of human aldehyde dehydrogenase 5 family, member
 PT ALDH5A1 gene for treating metabolic diseases and for expressing
 PT ALDH5A1 protein useful in identifying drugs to treat 4-hydroxybutyric
 PT aciduria -
 XX
 PS Claim 18; Page 15; 151pp; English.
 XX
 CC The invention describes an isolated polynucleotide comprising a
 CC nucleotide sequence which is a polymorphic variant of a reference
 CC sequence for the aldehyde dehydrogenase 5 family, member A1
 CC (succinate-semialdehyde dehydrogenase) (ALDH5A1) gene or its fragment.
 CC The polypeptide is useful for screening for drugs targeting it by
 CC contacting the ALDH5A1 polymorphic variant with a candidate agent and
 CC assaying for binding activity. The polypeptide and haplotypes are useful
 CC for identifying an association between a trait such as a clinical
 CC response to a drug targeting ALDH5A1 and a haplotype ALDH5A1 gene.
 CC Transgenic animals are also useful for studying expression of the ALDH5A1
 CC isoforms in vivo, for in vivo screening and testing of drugs against
 CC ALDH5A1 protein and for testing the efficacy of therapeutic agents and

CC compounds for 4-hydroxybutyric aciduria and metabolic diseases in a
 CC biological system. Antibodies are useful for diagnostic and prognostic
 CC formats and therapeutic methods, for immunoprecipitating the polypeptide
 CC from solution, for detecting ALDH5A1 protein isoforms in biological
 CC samples, frozen tissue sections, for use in immunocytochemical,
 CC immunohistochemical and immunofluorescence techniques. The polynucleotide
 CC is useful for gene therapy and antisense gene therapy. This sequence is
 CC a primer extension oligonucleotide used to detect polymorphisms in the
 CC ALDH5A1 gene described in the method of the invention.
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 U; 0 other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGGCCAGG 12
 Db 2 GGGCCAGG 9
 RESULT 225
 AAS95685
 ID AAS95685 standard; DNA; 10 BP.
 XX
 AC AAS95685;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Superoxide dismutase 1 (SOD1) allele-specific oligonucleotide #26.
 XX
 KW Superoxide dismutase 1; soluble amyotrophic lateral sclerosis 1 (adult);
 KW haplotyping; SOD1; allele-specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200185741-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 07-MAY-2001; 2001WO-US14772.
 XX
 PR 05-MAY-2000; 2000US-202491P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Choi JY, Bentivegna SC, Kiem SE, Koshy B, Parks KE;
 XX
 DR WPI; 2002-055578/07.
 XX
 PT Isolated human superoxide dismutase 1 (SOD1) soluble polynucleotide,
 PT useful for screening therapeutic compounds, comprises a sequence which
 PT is a polymorphic variant of reference sequence for the SOD1 gene or its
 PT fragment -
 XX
 PS Claim 17; Page 13; 70pp; English.
 XX
 CC The invention relates to an isolated human superoxide dismutase 1,
 CC soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1) polynucleotide
 CC (1) comprising a sequence which is a polymorphic variant of a reference
 CC sequence for the SOD1 gene. Haplotyping the SOD1 gene of an individual,
 CC involves: (a) determining whether the individual has one of the SOD1
 CC haplotypes or haplotype pairs given in the specification; or
 CC (b) determining for one copy of the SOD1 gene present in the individual,
 CC the identity of the nucleotide at two or more polymorphic sites selected
 CC from PS1-7. The method is useful for determining whether an individual
 CC has a haplotype or haplotype pairs defined in the specification. The
 CC method is also useful for improving the efficacy and reliability of
 CC several steps in the discovery and development of drugs for treating
 CC diseases associated with SOD1 activity, e.g., amyotrophic lateral
 CC sclerosis, and to validate SOD1 as a candidate agent for treating a
 CC specific condition or disease associated with SOD1 activity. It can
 CC further be used in the design of clinical trials of candidate drugs for

CC treating a specific condition or disease predicted to be associated with
 CC SOD1 activity. (1) is useful in studying the expression and function of
 CC SOD1, and in expressing SOD1 protein for use in screening for candidate
 CC drugs to treat diseases related to SOD1 activity. AAS9560-AAS95710
 CC represent human superoxide dismutase 1 soluble (amyotrophic lateral
 CC sclerosis 1 (adult)) (SOD1) allele-specific oligonucleotides and
 CC related PCR primers as described in the method of the invention.

XX Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Gaps 0;

Matches 8; Conservative 0; Indels 0; Gaps 0;
 QY 7 GCCAGGCC 14
 Db 1 GCCAGGCC 8

RESULT 226

ABL36370 standard; DNA; 10 BP.

XX ABL36370;

22-APR-2002 (first entry)

Human lysosomal acid phosphatase 2 primer-extension oligonucleotide 6.

XX Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11;
 XX lysosome-specific enzyme; orthophosphoric monoester hydrolysis;
 KW Hodgkin's disease; HD; acid phosphatase deficiency;
 KM novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism;
 KM transgenic animal; primer; probe; primer-extension oligonucleotide;
 KM SNP; single nucleotide polymorphism.

XX Homo sapiens.

XX WO200194362-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US18457.

XX 07-JUN-2000; 2000US-210047P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Klien SE, Messer C, Tanguay DA;

XX WPI; 2002-154563/20.

XX Novel genetic variants of acid phosphatase 2, lysosomal polypeptide
 PT gene useful in studying expression and function of the protein, and for
 PT screening drugs to treat diseases e.g. Hodgkin's disease -

XX Claim 19; Page 15; 1099P; English.

XX The invention comprises the human lysosomal acid phosphatase 2 (ACP2)
 CC nucleic acid and protein sequences. Specifically, the invention relates
 CC to the discovery of 22 novel polymorphic sites within the APC2 gene. The
 CC invention also comprises methods for haplotyping and genotyping the ACP2
 CC gene in an individual. The ACP2 gene (located on chromosome 11) encodes a
 CC lysosomal-specific enzyme that catalyses the hydrolysis of
 CC orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and
 CC protein are pharmaceutically important in the treatment of Hodgkin's
 CC disease (HD) and acid phosphatase deficiency. The novel ACP2 gene,
 CC polymorphisms of the invention are useful in haplotyping the ACP2 gene.
 CC ACP2 haplotyping is useful in validating ACP2 as a target (and designing
 CC drugs) for treating an ACP2-related disease or condition (e.g. Hodgkin's
 CC disease and acid phosphatase deficiency). The ACP2 gene polymorphisms are
 CC useful for ACP2 genotyping, which can also be used to develop diagnostic
 CC tests and therapeutic treatments. The ACP2 protein and nucleic acids of

CC the invention are useful in the production of a transgenic animal which
 CC expresses ACP2 protein. The ACP2 nucleic acids of the invention are
 CC useful in the production of allele-specific oligonucleotides designed to
 CC genotype each of the ACP2 polymorphisms. Nucleic acids ABL36299-ABL36320
 CC represent claimed ACP2 allele-specific probes. Nucleic acids ABL36321-
 CC ABL36364 represent claimed ACP2 allele-specific PCR primers. Nucleic
 CC acids ABL36365-ABL36408 represent claimed ACP2 primer-extension
 CC oligonucleotides.

XX Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Gaps 0;

Matches 8; Conservative 0; Indels 0; Gaps 0;
 QY 2 TCCGGGCC 9
 Db 3 TCCGGGCC 10

RESULT 227

ABL42760 standard; cDNA; 10 BP.

XX ABL42760;

12-APR-2002 (first entry)

Human maturation/activation dendritic cell expression gene tag #134.

XX Human; maturation/activation dendritic cell expression gene; tag;
 KW maturation; activation; dendritic cell; ss.

XX Homo sapiens.

XX JP2001327293-A.

XX 27-NOV-2001.

XX 22-MAY-2000; 2000JP-0150562.

XX 22-MAY-2000; 2000JP-0150562.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-127070/17.

XX Human maturation/activation dendritic cell expression gene group -

XX Claim 10; Page 12; 41P; Japanese.

XX The present invention describes a human maturation/activation dendritic
 CC cell (DC) expression gene group consisting of 100 genes which show the
 CC highest expression among the genes expressed in human maturation/
 CC activation DC. Also described are: (1) a protein expressed by the above
 CC human maturation/activation DC expression gene; (2) an antibody against
 CC the protein; and (3) an antagonist against the expression of each gene
 CC belonging to the above gene group. The gene group is useful for the
 CC treatment and the diagnosis of various human diseases related to human
 CC DC. ABL42627 to ABL42926 represent specifically claimed human
 CC maturation/activation DC expression gene tags from the present invention.

XX Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Gaps 0;

Matches 8; Conservative 0; Indels 0; Gaps 0;
 QY 9 CAGGCCAA 16
 Db 2 CAGGCCAA 9

RESULT 228
 ABL42855/c
 ID ABL42855 standard; cDNA: 10 BP.
 XX
 AC ABL42855;
 XX
 DT 12-APR-2002 (first entry)
 XX
 DE Human maturation/activation dendritic cell expression gene tag #229.
 XX
 KW Human; maturation/activation dendritic cell expression gene; tag;
 KM maturation; activation; dendritic cell; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2001327293-A.
 XX
 PD 27-NOV-2001.
 XX
 PF 22-MAY-2000; 2000JP-0150562.
 XX
 PR 22-MAY-2000; 2000JP-0150562.
 XX
 PA (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2002-127070/17.
 XX
 PT Human maturation/activation dendritic cell expression gene group -
 XX
 PS Claim 19; Page 15; 41pp; Japanese.
 XX
 CC The present invention describes a human maturation/activation dendritic
 CC cell (DC) expression gene group consisting of 100 genes which show the
 CC highest expression among the genes expressed in human maturation/
 CC activation DC. Also described are: (1) a protein expressed by the above
 CC human maturation/activation DC expression gene; (2) an antibody against
 CC the protein; and (3) an antagonist against the expression of each gene
 CC belonging to the above gene group. The gene group is useful for the
 CC treatment and the diagnosis of various human diseases related to human
 CC DC. ABL42627 to ABL42926 represent specifically claimed human
 CC maturation/activation DC expression gene tags from the present invention.
 CC
 SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CGGGCCAG 11
 DB 8 CGGGCCAG 1
 RESULT 229
 ABO81865
 ID ABO81865 standard; DNA: 11 BP.
 XX
 AC ABO81865;
 XX
 DT 19-NOV-2002 (first entry)
 XX
 DE Kaposi's Sarcoma SAGE library Tag No.15 SEQ ID NO:15.
 XX
 KW Human; Kaposi's sarcoma; tumour; angiogenesis; tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1225233-A2.
 XX
 PD 24-JUL-2002.
 XX
 PF 23-JAN-2002; 2002EP-0075264.
 XX

PR 23-JAN-2001; 2001EP-0200228.
 PR 28-SEP-2001; 2001EP-0203703.
 PR 28-SEP-2001; 2001US-325722P.
 XX
 PA (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
 XX
 PI Van Der Kuyt AC, Cornelissen M;
 XX
 DR WPI; 2002-668396/72.
 XX
 PT Determining presence of a tumor cell or angiogenesis, and the
 PT effectiveness of treatment, by detecting the presence of marker genes
 PT is useful to detect and monitor treatment of Kaposi's Sarcoma
 XX
 PS Claim 12; Page 8; 38pp; English.
 XX
 CC The present invention describes a method for determining if an individual
 CC has a tumour cell or site of angiogenesis, or if a treatment is effective
 CC in changing angiogenesis or changing a status of a set of target cells,
 CC comprising determining if a sample of the subject has an expression
 CC product of at least one marker gene. Also described is a compound capable
 CC of altering the expression or activity of Keratin 14, TIE 1, Sallodhesin
 CC or Siglec in a cell. Peripheral blood mononuclear cell (PBMC)-expressed
 CC Keratin 14, TIE 1, Sallodhesin or Siglec, and kits containing them from
 CC the present invention can be used in a diagnostic method, particularly as
 CC an indicator of angiogenesis or to determine presence of a tumour cell.
 CC The method of the invention is suitable to determine within a few days if
 CC a certain treatment against Kaposi's Sarcoma is successful. ABO81851 to
 CC ABO82006 represent nucleotide sequence used in the exemplification of the
 CC present invention.
 CC
 SQ Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;
 Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CGGGCCAGGCC 14
 DB 1 CAGGCCCTGGCC 11

RESULT 230
 ABV64637
 ID ABV64637 standard; cDNA: 11 BP.
 XX
 AC ABV64637;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 2423.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP15179.
 XX
 PR 03-JAN-2001; 2001DE-1000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining

PT homeostasis and identifying cosmetic or pharmaceutical agents against
 XX e.g. skin cancer -
 PS Disclosure; Page 92; 1345bp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC rosacea; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC ichthyosis; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.
 XX
 SQ Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 other;
 Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CCGGGCCAGCC 14
 1 CAGGCGCTGGCC 11
 Db
 RESULT 231
 ABV69138
 ID ABV69138 standard; cDNA; 11 BP.
 XX
 AC ABV69138;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 6924.
 XX
 KM Human: skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KM immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KM psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP15179.
 XX
 PR 03-JAN-2001; 2001DE-1000127.
 XX
 PA (HENKEL) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -
 XX
 PS Disclosure; Page 217; 1345bp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.
 XX
 SQ Sequence 11 BP; 0 A; 4 C; 5 G; 2 T; 0 other;
 Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 CCGGGCCAGCC 13
 1 CTGGGCGCTGGC 11
 Db
 RESULT 232
 ABQ86573
 ID ABQ86573 standard; cDNA; 11 BP.
 XX
 AC ABQ86573;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human skin stress/ageing related EST SEQ ID NO 328.
 XX
 KM Human: skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253773-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP15178.
 XX
 PR 03-JAN-2001; 2001DE-1000121.
 XX
 PA (HENKEL) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-528865/56.
 XX
 PT Identifying genes involved in skin stress and ageing, useful e.g. in
 PT screening for cosmetic or therapeutic agents, based on differential
 PT gene expression -
 XX
 PS Claim 8; Page 50; 325bp; German.
 CC The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention.
 XX
 SQ Sequence 11 BP; 0 A; 4 C; 5 G; 2 T; 0 other;
 Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 CCGGGCCAGCC 13
 1 CTGGGCGCTGGC 11
 Db

RESULT 233
ABZ72939/c
ID ABZ72939 standard; RNA; 12 BP.
XX
AC ABZ72939;
XX
DT 09-APR-2003 (first entry)
XX
DE Rod opsin hammerhead ribozyme oligonucleotide.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease;
KW target; ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Synthetic.
OS Homo sapiens.
PN WO200288320-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-US13679.
XX
PR 01-MAY-2001; 2001US-0847601.
XX
PA (UYFL) UNIV FLORIDA.
PI Lewin AS, Shaw LC, Grant MB;
XX
DR MPI; 2003-111880/10.
XX
PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration -
XX
PS Example 5; Page 73; 115pp; English.
XX
CC The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, inos,
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 12 BP; 3 A; 4 C; 4 G; 1 U; 0 other;
XX
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCCAGGCCAA 16
DB 11 GGCTGGCCTA 1
XX
RESULT 234
AAD03853/c
ID AAD03853 standard; DNA; 17 BP.
XX
AC AAD03853;
XX
DT 02-JUL-2001 (first entry)
XX
DE Human cell cycle checkpoint protein, hchk1 DNA amplifying PCR primer #2.
XX
KW Human; cell cycle checkpoint; chk1; tumour; malignancy;
KW cell growth inhibitor; development deficiency; PCR primer;
KW DNA damage; kinase; ss.
XX
OS Homo sapiens.
PN US6218109-B1.
XX
PD 17-APR-2001.
XX
PF 05-SEP-1997; 97US-0924183.
XX
PR 05-SEP-1997; 97US-0924183.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PI Elledge SJ, Sanchez Y;
XX
DR MPI; 2001-289827/30.
XX
PT New Chk1 proteins and gene sequences encoding the proteins useful as
PT probes for a portion of the chromosome associated with tumors and other
PT malignancies, growth and/or development deficiencies -
XX
PS Claim 17; Column 24; 37pp; English.
XX
CC The present sequence is a degenerate PCR primer used for amplifying the
CC human cell cycle checkpoint protein, hchk1 DNA. The cell cycle
CC checkpoints are regulatory pathways that control the order and timing of
CC cell cycle transitions, and ensure that critical events such as DNA
CC replication and chromosome segregation are completed with high fidelity.
CC The chk1 protein controls cell cycle in response to DNA damage. It
CC functions as kinase and phosphorylates the key regulators of Cdk tyrosine
CC phosphorylation. The checkpoint gene sequences are used as probes for a
CC portion of the chromosome associated with tumors and other malignancies,
CC as well as growth and/or development deficiencies. The chk1 proteins are
CC useful for generating specific antibodies and for inhibiting growth of
CC cells.
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;
XX
Query Match 39.0%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 GGCCAGGCCAA 16
DB 11 GGCTGGCCTCA 1
XX
RESULT 235
AAS18424/c
ID AAS18424 standard; DNA; 17 BP.
XX
AC AAS18424;
XX
DT 12-MAR-2002 (first entry)

```
XX DE Degenerate PCR primer #2 used to amplify DNA encoding human chk1.
XX
XX KM Human; checkpoint protein; hchk1; DNA damage; chromosome 11q24;
XX KM cell cycle checkpoint pathway; inhibition of cell growth; tumour;
XX KM malignancy; growth deficiency; development deficiency; PCR primer; ss.
XX OS Homo sapiens.
XX PN US6307015-B1.
XX PD 23-OCT-2001.
XX PF 12-JAN-2000; 2000US-0488364.
XX PR 05-SEP-1997; 97US-0924183.
XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX PI Elledge SJ, Sanchez Y;
XX DR WPI; 2002-040207/05.
XX
PT New mammalian checkpoint protein and gene, for generating specific
PT antibodies or for inhibiting the growth of cells, and for use as a
PT probe for a portion of a chromosome associated with tumours or
PT malignancies -
PS Example 1; Column 24; 39pp; English.
XX
CC The present invention relates to the isolation of human and mouse
CC checkpoint (chk1) proteins and the nucleic acid sequences encoding them.
CC Human chk1 (hchk1) maps to chromosome 11q24. Chk1 is involved in
CC cellular responses to DNA damage, in the cell cycle checkpoint pathway.
CC The protein is useful for generating specific antibodies and for
CC inhibiting the growth of cells. The nucleotide sequence encoding the
CC protein may be used as a probe for a portion of the chromosome
CC associated with tumours and other malignancies, as well as growth and/or
CC development deficiencies. The present sequence represents a degenerate
CC PCR primer used to amplify DNA encoding human chk1 protein.
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;
Query Match 39.0%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 GGCCAGGCCCA 16
Db 11 GGCTGTCCAA 1
RESULT 236
ABX16354/C
ID ABX16354 standard; DNA; 17 BP.
XX
XX AC ABX16354;
XX
XX DT 08-APR-2003 (first entry)
XX
XX DE Human checkpoint gene Chk1 PCR primer #2.
XX
XX KM Human; checkpoint; chk1; anti-Chk1 antibody; tumour;
XX KM PCR; primer; ss.
XX
XX OS Homo sapiens.
XX PN US2002156247-A1.
XX PD 24-OCT-2002.
XX PF 12-DEC-2001; 2001US-0020038.
XX
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```
PR 12-JAN-2000; 2000US-0488364.
XX
XX PA (ELLE/) ELLEDGE S J.
XX PA (SANC/) SANCHEZ Y.
XX
XX PI Elledge SJ, Sanchez Y;
XX DR WPI; 2003-182651/18.
XX
XX PT New anti-Chk1 antibody, that may be a monoclonal or polyclonal
XX PT antibody, useful for detecting a Chk1 protein that is associated with a
XX PT tumor -
XX
XX PS Example 1; Page 13; 28pp; English.
XX
CC The invention describes an anti-Chk1 antibody capable of specifically
CC binding to an antigenic determinant on the proteins encoded by a
CC sequence comprising 476 (3 sequences), 479, 496 or 513 amino acids.
CC A new method is used to produce the antibody, which is useful for
CC detecting a Chk1 protein that is associated with a tumour. This
CC sequence represents a PCR primer used to isolate DNA encoding the
CC human checkpoint protein Chk1.
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;
Query Match 39.0%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 GGCCAGGCCCA 16
Db 11 GGCTGTCCAA 1
RESULT 237
AAK29342
ID AAK29342 standard; DNA; 20 BP.
XX
XX AC AAK29342;
XX
XX DT 10-JUN-1999 (first entry)
XX
XX DE Chemically modified sense control probe ISIS No: 14318.
XX
XX KM Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
XX KM JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
XX KM hyperproliferative disease; human; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO90909214-A1.
XX
XX PD 25-FEB-1999.
XX
XX PF 07-AUG-1998; 98WO-US16488.
XX
XX PR 13-AUG-1997; 97US-0910629.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Dean N, Gaarde WA, McKay R, Monia BP, Nero PS;
XX DR WPI; 1999-181060/15.
XX
XX PT New antisense oligonucleotides that detect and modulate the
XX PT expression of Jun N-terminal kinase proteins - useful for treating
XX PT hyperproliferative diseases and inhibiting tumor growth in animals,
XX PT and for modulating protein phosphorylation by these proteins
XX
XX PS Example 4; Page 92; 190pp; English.
XX
XX CC The invention relates to antisense oligonucleotides that detect and
```

CC modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC oligonucleotides specifically hybridize to a nucleic acid encoding a
CC JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC proteins. The oligonucleotides are useful for modulating JNK protein
CC expression and cell cycle progression in cultured cells or animal cells.
CC The oligonucleotides are also useful for modulating the phosphorylation
CC of a protein that has been phosphorylated by a JNK protein, and the
CC expression of a cellular protein that promotes one or more metastatic
CC events. The oligonucleotides also form pharmaceutical compositions for
CC treating animals with a hyperproliferative disease, and for inhibiting
CC tumor growth in an animal.
XX
SQ Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;
Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GTCCGGGCGCAGCC 14
Db 7 GGCCTGGCCCGGAC 20
RESULT 239
AAC62874/C
ID AAC29331 standard; DNA; 20 BP.
XX AAC29331;
AC AAC29331;
XX 10-JUN-1999 (first entry)
DT
XX
DE JNK2-specific probe ISIS No: 12560.
XX
XX Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
KW JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
KM hyperproliferative disease; human; ss.
XX
OS Synthetic.
XX Homo sapiens.
XX WO9909214-A1.
XX 25-FEB-1999.
PD
XX
PF 07-AUG-1998; 98WO-US16488.
XX
PR 13-AUG-1997; 97US-0910629.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean N, Gaarde WA, McKay R, Monia BP, Nero PS;
XX
DR WPI; 1999-181060/15.
XX
XX
PT New antisense oligonucleotides that detect and modulate the
PT expression of Jun N-terminal kinase proteins - useful for treating
PT hyperproliferative diseases and inhibiting tumor growth in animals,
PT and for modulating protein phosphorylation by these proteins
XX
PS Example 4; Page 87; 190pp; English.
XX
XX The invention relates to antisense oligonucleotides that detect and
CC modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC oligonucleotides specifically hybridize to a nucleic acid encoding a
CC JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC proteins. The oligonucleotides are useful for modulating JNK protein
CC expression and cell cycle progression in cultured cells or animal cells.
CC The oligonucleotides are also useful for modulating the phosphorylation
CC of a protein that has been phosphorylated by a JNK protein, and the
CC expression of a cellular protein that promotes one or more metastatic
CC events. The oligonucleotides also form pharmaceutical compositions for
CC treating animals with a hyperproliferative disease, and for inhibiting
CC tumor growth in an animal.

XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GTCCGGGCGCAGCC 14
Db 14 GGCCTGGCCCGGAC 1
RESULT 239
AAC62874/C
ID AAC62874 standard; DNA; 20 BP.
XX AAC62874;
AC AAC62874;
XX 06-FEB-2001 (first entry)
DT
XX
DE JNK antisense oligonucleotide ISIS #12560.
XX
XX Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
KW cellular hyperproliferation; Alzheimer's; Parkinson's disease;
KW amyotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
KW myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
KW diabetes; Jun N-terminal kinase; ss.
XX
OS Homo sapiens.
XX WO200059549-A1.
XX 12-OCT-2000.
PD
XX
PF 04-APR-2000; 2000WO-US08880.
XX
PR 07-APR-1999; 99US-0287796.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI McKay R, Dean NM, Monia BP, Nero PS, Gaarde WA;
XX
DR WPI; 2000-638427/61.
XX
XX
XX Novel methods for reducing apoptosis comprising contacting cells with
PT antisense oligonucleotides, useful for treating apoptotic disorders,
PT e.g. cancer -
XX
PS Claim 3; Page 133; 160pp; English.
XX
XX The present invention relates to antisense oligonucleotides
CC (AAC62844-C63000, AAA96093-A96099 and AAA07993) that hybridise
CC specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
CC protein, resulting in decrease of JNK2 expression and leading to
CC induction of apoptosis. The present sequence is one such antisense
CC oligonucleotide. The oligonucleotides of the present invention are useful
CC for treating diseases or conditions with reduced apoptosis, e.g. cancer
CC and cellular hyperproliferation. The oligonucleotides may also be used to
CC increase the stimulation of apoptotic proteins, e.g. for treating
CC Alzheimer's or Parkinson's disease, amyotrophic lateral sclerosis,
CC retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
CC obstructive jaundice, polycystic kidney and diabetes. The present
CC sequence may have a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GTCCGGGCGCAGCC 14
Db 14 GGCCTGGCCCGGAC 1

```

RESULT 240
AAC62885
ID AAC62885 standard; DNA: 20 BP.
XX
XX AAC62885;
AC AAC62885;
DT 06-FEB-2001 (first entry)
XX
XX JNK antisense oligonucleotide ISIS #14318.
DE
XX Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
XX cellular hyperproliferation; Alzheimer's; Parkinson's disease;
XX amyotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
XX myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
XX diabetes; Jun N-terminal kinase; ss.
XX Homo sapiens.
XX MO200059549-A1.
XX 12-OCT-2000.
XX 04-APR-2000; 2000MO-US08880.
XX 07-APR-1999; 99US-0287796.
XX (ISIS-) ISIS PHARM INC.
XX Mckay R, Dean NM, Monia BP, Nero PS, Gaarde WA;
XX WPI; 2000-638427/61.
XX
XX Novel methods for reducing apoptosis comprising contacting cells with
XX antisense oligonucleotides, useful for treating apoptotic disorders,
XX e.g. cancer -
XX
XX Example 4; Page 135; 160pp; English.
XX
XX The present invention relates to antisense oligonucleotides
XX (AAC62884-C63000, AAA66093-A66099 and AAA07993) that hybridise
XX specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
XX protein, resulting in decrease of JNK2 expression and leading to
XX induction of apoptosis. The present sequence is one such antisense
XX oligonucleotide. The oligonucleotides of the present invention are useful
XX for treating diseases or conditions with reduced apoptosis, e.g. cancer
XX and cellular hyperproliferation. The oligonucleotides may also be used to
XX increase the stimulation of apoptotic proteins, e.g. for treating
XX Alzheimer's or Parkinson's disease, amyotrophic lateral sclerosis,
XX retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
XX obstructive jaundice, polycystic kidney and diabetes. The present
XX sequence may have a phosphorothioate backbone.
XX
XX Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;
SQ
Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GTCGGGCGCCAGCC 14
DB 7 GGCCTGGCGCGGAC 20
RESULT 241
AAA48651/C
ID AAA48651 standard; DNA: 20 BP.
XX
XX AAA48651;
AC AAA48651;
XX
XX 20-SEP-2000 (first entry)
DT
XX

```

```

DE Antisense oligonucleotide ISIS no.15354 to human JNK2 gene.
XX
XX Antisense; E-selectin; TNF alpha; cell adhesion;
XX tumour necrosis factor alpha; phosphorothioate; methoxyethoxy;
XX sepsis; rheumatoid arthritis; inflammatory; immune disease;
XX inflammatory bowel disease; allergic contact dermatitis; psoriasis;
XX diabetes; Grave's disease; allograft rejection; cancer; antibacterial;
XX immunosuppressive; antipsoriatic; antidiabetic; antithyroid;
XX cytostatic; dermatological; antiallergic; Ha-ras; c-ras;
XX c-Jun N-terminal kinase; JNK; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..6
XX /tag= a
XX /mod_base= OTHER
XX /note= "All bases are 2'-methoxyethoxy,
XX additionally C bases are m5c"
XX modified_base 7..15
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate internucleotide linkage"
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "All bases are 2'-methoxyethoxy,
XX additionally C bases are m5c"
XX
XX MO200034303-A1.
XX
XX 15-JUN-2000.
XX
XX 08-DEC-1999; 99MO-US28965.
XX
XX 10-DEC-1998; 98US-0209668.
XX
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Xu XS;
XX WPI; 2000-423367/36.
XX
XX Modulating cell adhesion molecule expression for treating immune or
XX inflammatory diseases involves treating cell with specific inhibitor of
XX Tumour Necrosis Factor alpha signalling molecule -
XX
XX Claim 36; Page 46; 100pp; English.
XX
XX A novel method for modulating cell adhesion molecule expression
XX involves antisense inhibition of a tumour necrosis factor (TNF) alpha
XX signalling molecule. In the method TNF alpha signalling molecules
XX Ha-ras, c-ras and c-Jun N-terminal kinase (JNK)2 were inhibited by
XX antisense oligonucleotides. In addition an antisense oligonucleotide
XX to the cell adhesion molecule E-selectin was also examined. The
XX present sequence is the JNK2 antisense oligonucleotide. The
XX antisense oligonucleotides used in the method contained modifications,
XX namely phosphorothioate linkages and 2'methoxyethoxy bases. Some C
XX residues also had a 5'methyl modification. Inhibitors of the TNF alpha
XX signalling molecules have antibacterial, immunosuppressive,
XX antipsoriatic, antidiabetic, antithyroid, cytostatic, dermatological,
XX anti-allergic and anti-inflammatory activity. The antisense inhibitors
XX may be useful for the treatment of sepsis, rheumatoid arthritis,
XX inflammatory, immune disease, inflammatory bowel disease, allergic
XX contact dermatitis, psoriasis, diabetes, Grave's disease, allograft
XX rejection and cancer.
XX
XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
SQ
Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 GTCCGGCCAGGCC 14
 DB 14 GGCTGCGCCGAC 1

RESULT 242
 AAH23754/c
 AAH23754 standard; DNA: 20 BP.

AAH23754;
 13-AUG-2001 (first entry)

JNK1 antisense oligonucleotide, JNK2AS, (ISIS #12560).

JNK, Jun kinase, antisense; cytosolic; cancer;
 2'-O-methoxyethyl oligonucleotide; MOE; phosphorothioate; ss.
 Synthetic.

Key Location/Qualifiers
 modified_base 1..20
 /tag= a
 /mod_base= "OTHER"
 /note= "This oligonucleotide is a 2'-O-methoxyethyl (MOE) chimeric antisense oligonucleotide containing five MOE/phosphodiester residues flanking a 2'-deoxynucleotide/phosphorothioate region"

MO200134792-A2.
 17-MAY-2001.

10-NOV-2000; 2000MO-US30869.
 12-NOV-1999; 99US-0165224.

(USSH) US DEPT HEALTH & HUMAN SERVICES.
 Petapova O, Gorospe M, Holbrook NJ;
 WPI; 2001-335925/35.

Use of Jun Kinase antisense mRNA for treating cancer by administering vector comprising promoter operably linked to DNA sequence that encodes the antisense mRNA to patient diagnosed with cancer

Claim 1; Page 41; 75pp; English.

The present invention relates to the use of Jun Kinase (JNK) antisense oligonucleotides for treating cancer and for screening compounds that mimic or augment the effect of JNK antisense oligonucleotides treatment for cancer. The present sequence is one such JNK antisense oligonucleotide.

Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

Query Match 38.0%; Score 7.6; DB 1; Length 20;
 Best Local Similarity 71.4%; Pred. No. 2.3e+02;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCC 14
 DB 14 GGCTGCGCCGAC 1

RESULT 243
 AAF99183/c
 AAF99183 standard; DNA: 20 BP.
 AAF99183;
 12-JUN-2001 (first entry)

XX XX
 DE Immunostimulatory nucleic acid #299.
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW Immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 OS Synthetic.
 PN WO200122972-A2.
 PD 05-APR-2001.

PF 25-SEP-2000; 2000MO-US26383.
 XX 25-SEP-1999; 99US-0156113.
 PR 27-SEP-1999; 99US-0156135.
 PR 23-AUG-2000; 2000US-0227436.
 XX
 PA (TOMA) UNIT TOMA RES. FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 PI Kriegl AM, Schetter C, Vollmer J;
 WPI; 2001-273485/28.

Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids

Claim 101; Page 44; 338pp; English.

The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acid can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a T12 to a Th1 immune response and to activate immune cells.

Note: the present sequence may have a phosphorothioate backbone.

Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

Query Match 38.0%; Score 7.6; DB 1; Length 20;
 Best Local Similarity 71.4%; Pred. No. 2.3e+02;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCC 14
 DB 14 GGCTGCGCCGAC 1

RESULT 244
 ABS77827/c
 ABS77827 standard; DNA: 20 BP.
 ABS77827;
 13-DEC-2002 (first entry)

Angiogenesis inhibitory oligonucleotide #111.

Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis;
 KW psoriasis; diabetic retinopathy; retinopathy of prematurity;
 KW macular degeneration; corneal graft rejection; neovascular glaucoma;
 KW retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;

KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
KW haemophilic joint; angiodioma; wound granulation;
KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
OS Synthetic.
PN WO200253141-A2.
XX
XX 11-JUL-2002.
PD
XX
PF 14-DEC-2001; 2001WO-US48458.
XX
XX 14-DEC-2000; 2000US-255534P.
PR
XX (COLE-) COLEY PHARM GROUP INC.
PA
XX Bratzler RL;
PI
XX WPI; 2002-566690/60.
DR
XX
XX Inhibiting angiogenesis in a subject, involves administering at least
PT one antiangiogenic nucleic acid molecule to the subject -
PS
XX Claim 2; Page 25; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule.
CC Also included is a kit comprising a first container housing the
CC antiangiogenic nucleic acids, and instructions for administering them to
CC a subject having a condition characterised by unwanted angiogenesis.
CC The method is useful for inhibiting angiogenesis associated with solid
CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid
CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
CC macular degeneration, corneal graft rejection, neovascular glaucoma,
CC retrolental fibroplasia, rubecosis, Osler-Weber Syndrome, myocardial
CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
CC joints, angiodioma, wound granulation, intestinal adhesions,
CC atherosclerosis, scleroderma and hypertrophic scars. The present
CC sequence is an antiangiogenic nucleic acid of the invention.
SQ
XX
XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
QY
XX
XX Query Match 38.0%; Score 7.6; DB 1; Length 20;
XX Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Db Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
1 GTCCGGGCCAGGCC 14
14 GGCTTGCCCCGAC 1

RESULT 245
ABL39057/C
ID ABL39057 standard; DNA; 20 BP.
XX
XX ABL39057;
AC
XX
XX 16-APR-2002 (first entry)
DT
XX
XX Immunostimulatory nucleic acid SEQ ID NO: 463.
DE
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /+tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
XX WO200197843-A2.
PN

XX
XX 27-DEC-2001.
PD
XX
XX 22-JUN-2001; 2001WO-US20154.
PF
XX
XX 22-JUN-2000; 2000US-213346P.
PR
XX (IOWA) UNIV IOWA RES FOUND.
PA
XX
XX Weiner G, Hartmann G;
PI
XX WPI; 2002-154611/20.
DR
XX
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer -
XX
XX
XX Disclosure; Page 212; 312pp; English.
XX
XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in
CC the exemplification of the invention.
SQ
XX
XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
QY
XX
XX Query Match 38.0%; Score 7.6; DB 1; Length 20;
XX Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Db Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
1 GTCCGGGCCAGGCC 14
14 GGCTTGCCCCGAC 1

RESULT 246
AAX54706/C
ID AAX54706 standard; DNA; 9 BP.
XX
XX AAX54706;
AC
XX
XX 05-JUL-1999 (first entry)
DT
XX
XX Human fibronectin antisense oligonucleotide fragment.
DE
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
XX Synthetic.
OS
XX
XX MO9913886-A1.
PN
XX
XX 25-MAR-1999.
PD
XX

PF 17-SEP-1998; 98WO-US19419.
 XX
 PR 09-JUN-1998; 98US-0093972.
 PR 17-SEP-1997; 97US-0059160.
 PA (UYEC-) UNIV EAST CAROLINA.
 PI NYCE JW;
 PT WPI; 1999-229400/19.
 DR New antisense oligonucleotides used in treatment of, e.g. pulmonary
 XX vasoconstriction
 PT
 PS Disclosure; Page 55; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (AA52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences AAX55272-74. These multiple target
 CC oligonucleotides (specifically AAX5180-271) can be used for the
 CC antisense treatment of diseases and conditions. Typical diseases and
 CC conditions are those associated with impaired respiration and
 CC inflammation, including lung diseases, pulmonary vasoconstriction,
 CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impaired
 CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
 CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
 CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
 CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
 CC hepatic metastases, as well as all types of cancers which metastasize
 CC or have metastasized to the lungs, including breast and prostate cancer.
 CC
 SQ Sequence 9 BP; 0 A; 4 C; 5 G; 0 U; 0 other;
 QY Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Db Best Local Similarity 88.9%; Pred. No. 5.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 GTCCGGGCC 9
 9 GCCCGGGCC 1
 RESULT 247
 AAF20275/C
 ID AAF20275 standard; DNA; 9 BP.
 AC AAF20275;
 XX
 DT 14-MAR-2001 (first entry)
 DE Human fibronectin polynucleotide fragment #1842.
 XX
 KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antiaesthetic; hypotensive; cytostatic;
 KM surfactant hypoproduction; pulmonary obstruction; impeded respiration;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200062736-A2.
 XX

PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000MO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PI NYCE J W.
 PT NYCE JW;
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 PS Claim 14; Page 220; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergies
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 CC
 SQ Sequence 9 BP; 0 A; 4 C; 5 G; 0 U; 0 other;
 QY Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Db Best Local Similarity 88.9%; Pred. No. 5.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 GTCCGGGCC 9
 9 GCCCGGGCC 1
 RESULT 248
 AAA34153/C
 ID AAA34153 standard; DNA; 9 BP.
 AC AAA34153;
 XX
 DT 28-JUL-2000 (first entry)
 DE Human adenosine receptor related polynucleotide SEQ ID NO:1842.
 XX
 KM Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KM phosphorothioate; impaired respiration; inflammation; allergy;
 KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KM

XX anti-allergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Disclosure; Page 495; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA3312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 185, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA3233 to AAA33992) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.
 XX
 XX Sequence 9 BP; 0 A; 4 C; 5 G; 0 U; 0 other;
 SQ
 QY Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Db Best Local Similarity 88.9%; Pred. No. 5.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTCCGGGGCC 9
 Db 9 GCCCGGGGCC 1
 RESULT 249
 ABQ71850
 ID ABQ71850 standard; DNA; 9 BP.
 XX
 AC ABQ71850;
 XX
 DT 28-AUG-2002 (first entry)
 XX

XX Zinc finger protein related oligonucleotide target SEQ ID NO:2148.
 DE
 XX
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200242459-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 20-NOV-2001; 2001WO-US43438.
 XX
 PR 20-NOV-2000; 2000US-0716637.
 XX
 PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX
 PI Liu Q;
 XX
 DR WPI; 2002-500284/53.
 XX
 PT New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering.
 PT comprises first, second and third zinc fingers, ordered from N- to
 PT C-terminus -
 XX
 PS Example 1; Page 56; 81pp; English.
 XX
 CC The present invention describes a zinc finger protein (I) that binds to
 CC a target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target site. Also described are: (1) a polypeptide
 CC (II) comprising (1); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
 CC it binds to the S1 target site, selecting the F2 zinc finger such
 CC that it binds to the S2 target site, and selecting the F3 zinc
 CC finger such that it binds to the S3 target site, thus designing (I)
 CC that binds to a target site. (I) is useful for recognition of triplet
 CC target sites having the nucleotide G in the 5'-most position of the
 CC substrate. (I) is useful in studying gene function, and for human
 CC therapeutics and plant engineering. (I), (II) or (III) is useful in
 CC therapeutic methods to modulate the expression of a target region within
 CC a subject, in diagnostic methods for sequence specific detection of
 CC target nucleic acid in a sample, and in assays to determine the
 CC phenotype and function of gene expression. (I) has improved affinity
 CC and specificity for their target sequences, as well as enhanced
 CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
 CC represent DNA target sequences and zinc finger peptides which are given
 CC in the exemplification of the present invention.
 XX
 XX Sequence 9 BP; 1 A; 2 C; 6 G; 0 U; 0 other;
 SQ
 QY Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Db Best Local Similarity 88.9%; Pred. No. 5.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GGCGCCAGGC 13
 Db 1 GGCGCCAGGC 9
 RESULT 250
 ABQ71851
 ID ABQ71851 standard; DNA; 9 BP.
 XX
 AC ABQ71851;
 XX
 DT 28-AUG-2002 (first entry)
 XX
 DE Zinc finger protein related oligonucleotide target SEQ ID NO:2149.
 XX

XX	Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX	Homo sapiens.
OS	Synthetic.
XX	MO200242459-A2.
XX	
XX	30-MAY-2002.
PD	
PF	20-NOV-2001; 2001WO-US43438.
XX	
PR	20-NOV-2000; 2000US-0716637.
XX	
PA	(SANG-) SANGAMO BIOSCIENCES INC.
PI	
LI	Liu Q;
DR	WPI; 2002-500284/53.
XX	
PT	New zinc finger protein that binds to target site, useful in studying
PT	gene function and for human therapeutics and plant engineering,
PT	comprises first, second and third zinc fingers, ordered from N- to
PT	C-terminus -
XX	
PS	Example 1; Page 56; 81pp; English.
XX	
CC	The present invention describes a zinc finger protein (I) that binds to
CC	a target site, comprising a first (F1), a second (F2), and a third (F3)
CC	zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC	target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC	and a third (S3) target sub-site. Also described are: (i) a polypeptide
CC	(II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC	(3) designing (M) (I) involves selecting the F1 zinc finger such that
CC	it binds to the S1 target sub-site, selecting the F2 zinc finger such
CC	that it binds to the S2 target sub-site, and selecting the F3 zinc
CC	finger such that it binds to the S3 target sub-site, thus designing (I)
CC	that binds to a target site. (I) is useful for recognition of triplet
CC	target substrates having the nucleotide G in the 5'-most position of the
CC	sub-site. (I) is useful in studying gene function, and for human
CC	therapeutics and plant engineering. (I), (II) or (III) is useful in
CC	therapeutic methods to modulate the expression of a target region within
CC	a subject, in diagnostic methods for sequence specific detection of
CC	target nucleic acid in a sample, and in assays to determined the
CC	phenotype and function of gene expression. (I) has improved affinity
CC	and specificity for their target sequences, as well as enhanced
CC	biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC	represent DNA target sequences and zinc finger peptides which are given
CC	in the exemplification of the present invention.
XX	
XX	Sequence 9 BP; 1 A; 2 C; 6 G; 0 U; 0 other;
QY	
Db	5 GGCGCAGGC 13
	1 GGCGCAGGC 9
QY	
Db	1 GGCGCAGGC 9
XX	
RESULT 251	
AAZ82328	
ID	AAZ82328 standard; DNA; 10 BP.
XX	
AC	AAZ82328;
XX	
DT	07-APR-2000 (first entry)
XX	
DE	Metastatic breast tumour cell upregulated transcript tag #1562.
XX	
XX	Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KM	non-metastatic breast tumour tissue; gene therapy; anticancer;
KM	antimetastatic; vaccine; diagnosis; ss.

XX	Homo sapiens.
OS	
XX	
PN	W0965928-A2.
XX	
PD	23-DEC-1999.
XX	
PF	18-JUN-1999; 99MO-US13647.
XX	
PR	19-JUN-1998; 98US-0089853.
XX	
PR	19-JUN-1998; 98US-0089997.
XX	
PR	19-JUN-1998; 98US-0090039.
XX	
PR	19-JUN-1998; 98US-0090040.
XX	
PR	19-JUN-1998; 98US-0090041.
XX	
PA	(GENZ) GENZYME CORP.
XX	
PA	(ROBE/) ROBERTS B.L.
XX	
PA	(SHAN/) SHANKARA S.
XX	
P1	Roberts BL, Shankara S;
XX	
DR	WPI: 2000-106079/09.
XX	
PT	Isolated polynucleotides differentially expressed between metastatic
XX	
PT	and non-metastatic breast cancer cells, useful for diagnosis,
XX	
PT	prevention and treatment of cancer
XX	
PS	Claim 1; Page 100; 21pp; English.
XX	
CC	AA80767 to AA83941 represent tags corresponding to distinct
XX	
CC	transcripts that are preferentially transcribed in the metastatic breast
XX	
CC	tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
XX	
CC	AA83942 to AA86677 represent tags corresponding to distinct transcripts
XX	
CC	that are preferentially transcribed in the primary or non-metastatic
XX	
CC	breast tumour tissue (i.e. are downregulated in metastatic breast tumour
XX	
CC	cells). These transcripts can be used for diagnosis, prognosis,
XX	
CC	monitoring and treatment of breast cancer, particularly where metastatic.
XX	
CC	Diagnosis is by standard immunoassays or hybridisation/amplification
XX	
CC	reactions. Compounds that modulate expression of the transcripts are
XX	
CC	potentially useful for treatment of (metastatic) breast cancer, while
XX	
CC	promoters from the transcripts are used to direct expression, in selected
XX	
CC	cell types, of e.g. therapeutic genes (also ribozymes or antisense
XX	
CC	sequences), particularly an antigen-encoding sequence for use in gene or
XX	
CC	cell-based vaccines. Polypeptides encoded by the transcripts are also
XX	
CC	useful in vaccines; for diagnosing breast cancer and for raising
XX	
CC	specific antibodies (Ab). Ab are used to detect the polypeptides or as
XX	
CC	therapeutic agents. Host cells that produce the polypeptides can be used
XX	
CC	to expand and isolate populations of educated, antigen-specific immune
XX	
CC	effector cells, e.g. cytotoxic T lymphocytes, and these used for
XX	
CC	adoptive immunotherapy.
XX	
SQ	Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;
XX	
Query Match	37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity	88.9%; Pred. No. 1.4e+02;
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX	
OY	6 GGCCAGGCC 14
XX	
DB	1 GGCTTGCC 9
XX	
RESULT 252	
ID	AA27977 standard; DNA, 10 BP.
XX	
AA27977;	
XX	
AC	
XX	
DT	10-APR-2000 (first entry)
XX	
DB	Human dendritic cell SAGE tag, SEQ ID NO:405.
XX	
FW	SAGE tag; serial analysis of gene expression; antigen-presenting cell;

KW APC; monocytic-derived dendritic cell; differential gene expression;
KM immunostimulatory cofactor; costimulatory factor; CTL;
KM cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13800.
XX
XX 19-JUN-1998; 98US-0089833.
PR 19-JUN-1998; 98US-0089844.
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089878.
PR 19-JUN-1998; 98US-0089911.
PR 19-JUN-1998; 98US-0089922.
PR 19-JUN-1998; 98US-0089933.
PR 19-JUN-1998; 98US-0089994.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0089999.
PR 19-JUN-1998; 98US-0090000.
PR 19-JUN-1998; 98US-0090035.
PR 19-JUN-1998; 98US-0090036.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
PR 19-JUN-1998; 98US-0090042.
PR 19-JUN-1998; 98US-0090043.
PR 19-JUN-1998; 98US-0090044.
PR 19-JUN-1998; 98US-0090045.
PR 19-JUN-1998; 98US-0090047.
PR 19-JUN-1998; 98US-0090048.
PR 19-JUN-1998; 98US-0090072.
PR 19-JUN-1998; 98US-0090076.
PR 19-JUN-1998; 98US-0090077.
PR 19-JUN-1998; 98US-0090078.
PR 19-JUN-1998; 98US-0090079.
PR 19-JUN-1998; 98US-0090080.
PR 08-DEC-1998; 98US-0111715.
XX
PA (GENZ) GENZYME CORP.
PA (ROBEZ) ROBERTS B L.
PA (SHAN/) SHANKARA S.
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer -
XX
XX Claim 1; Page 76; 130pp; English.
XX
XX Sequences AA27573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocytic-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or
XX ESTs (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can
XX lyse the tumour cells. Immunostimulatory cofactors also being required
XX for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen; to modulate the genotype of an APC; to screen

CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell
CC differentially expressed genes, or of their encoded proteins, can be used
CC to identify cells as belonging to the monocytic lineage. Cells containing
CC these genes can be used in active immunotherapy (or to stimulate
CC production of a population of antigen-specific effector cells) and
CC vectors containing them are used in gene therapy. Co-administration of
CC tumour antigens and APC-associated costimulatory factors ensures adequate
CC antigen presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC recruitment of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells.
XX
SQ Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;
XX
QY 5 GGGCCAGGC 13
Db 2 GGGCCTGGC 10
XX
XX Query Match 37.0%; Score 7.4; DB 1; Length 10;
XX Best Local Similarity 88.9%; Pred. No. 1.4e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
RESULT 253
AA284966 standard; DNA; 10 BP.
XX
XX AA284966;
AC
XX 07-APR-2000 (first entry)
DT
XX
XX Metastatic breast tumour cell downregulated transcript tag #4200.
DE
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KM non-metastatic breast tumour tissue; gene therapy; anticancer;
KM antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO965928-A2.
XX
XX 23-DEC-1999.
PD
XX
XX 18-JUN-1999; 99WO-US13647.
PF
XX
XX 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
XX
XX (GENZ) GENZYME CORP.
XX (ROBEZ) ROBERTS B L.
XX (SHAN/) SHANKARA S.
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic
XX PT and non-metastatic breast cancer cells, useful for diagnosis,
XX prevention and treatment of cancer -
XX
XX Claim 1; Page 171; 219pp; English.
XX
XX AA280767 to AA283941 represent tags corresponding to distinct
XX transcripts that are preferentially transcribed in the metastatic breast
XX CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
XX CC AA283942 to AA286677 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the primary or non-metastatic

CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cell). These transcripts can be used for diagnosis, prognosis, metastatic.
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from these transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines; for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 CC
 SQ Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 other;
 QY Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 5 CGGCGCAGC 13
 2 CGGCGCTGCG 10
 RESULT 254
 AAH76342
 ID AAH76342 standard; DNA; 10 BP.
 XX
 AC AAH76342;
 XX
 DT 29-OCT-2001 (first entry)
 XX
 DE 2. mays Ms45 promoter deletion mutant fragment LS02.
 XX
 KM Ms45; male tissue; regulatory region; transcription; male fertility;
 XX hybrid seed; promoter; ss.
 XX
 OS Zea mays.
 XX
 PN WO200160997-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 13-FEB-2001; 2001WO-US04527.
 XX
 PR 15-FEB-2000; 2000US-0504487.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL,
 DR WPI; 2001-514772/56.
 XX
 PT A male tissue-preferred regulatory region comprising nucleotide
 PT sequences essential for initiating transcription of the Ms45 gene
 PT useful for mediating fertility in a male plant -
 XX
 PS Example 5; Fig 8; 50pp; English.
 CC
 CC The invention provides a male tissue-preferred regulatory region (I)
 CC comprising nucleotide sequences essential for initiating transcription
 CC of the Ms45 gene. A method of mediating male fertility in a plant is
 CC provided that involves introducing an expression vector comprising a
 CC promoter operably linked to (I) into a plant where the exogenous gene
 CC impacts male fertility of the plant and (I) controls expression of the
 CC exogenous gene. A method of producing hybrid seeds is also provided.
 CC Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
 CC promoter region, used for determining the essential region of Ms45
 CC promoter.

XX
 SQ Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;
 QY Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 3 CGGCGCCAG 11
 2 CGGCGCCCG 10
 RESULT 255
 AAH76345/C
 ID AAH76345 standard; DNA; 10 BP.
 XX
 AC AAH76345;
 XX
 DT 29-OCT-2001 (first entry)
 XX
 DE Z. mays Ms45 promoter deletion mutant fragment LS05.
 XX
 KM Ms45; male tissue; regulatory region; transcription; male fertility;
 XX hybrid seed; promoter; ss.
 XX
 OS Zea mays.
 XX
 PN WO200160997-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 13-FEB-2001; 2001WO-US04527.
 XX
 PR 15-FEB-2000; 2000US-0504487.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL,
 DR WPI; 2001-514772/56.
 XX
 PT A male tissue-preferred regulatory region comprising nucleotide
 PT sequences essential for initiating transcription of the Ms45 gene
 PT useful for mediating fertility in a male plant -
 XX
 PS Example 5; Fig 8; 50pp; English.
 CC
 CC The invention provides a male tissue-preferred regulatory region (I)
 CC comprising nucleotide sequences essential for initiating transcription
 CC of the Ms45 gene. A method of mediating male fertility in a plant is
 CC provided that involves introducing an expression vector comprising a
 CC promoter operably linked to (I) into a plant where the exogenous gene
 CC impacts male fertility of the plant and (I) controls expression of the
 CC exogenous gene. A method of producing hybrid seeds is also provided.
 CC Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
 CC promoter region, used for determining the essential region of Ms45
 CC promoter.
 CC
 SQ Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;
 QY Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 3 CGGCGCCAG 11
 9 CGGCGCCCG 1
 RESULT 256
 AAH76348
 ID AAH76348 standard; DNA; 10 BP.
 XX

```
AC AAH76348;
XX
DT 29-OCT-2001 (first entry)
XX
DE Z. mays Ms45 promoter deletion mutant fragment LS08.
XX
KM Ms45; male tissue; regulatory region; transcription; male fertility;
KW hybrid seed; promoter; ss.
XX
OS Zea mays.
XX
PN W0200160997-A2.
XX
PD 23-AUG-2001.
XX
PF 13-FEB-2001; 2001MO-US04527.
XX
PR 15-FEB-2000; 2000US-0504487.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX WPI; 2001-514772/56.
XX
PT A male tissue-preferred regulatory region comprising nucleotide
XX sequences essential for initiating transcription of the Ms45 gene
XX useful for mediating fertility in a male plant -
XX
PS Example 5; Fig 8; 50pp; English.
XX
CC The invention provides a male tissue-preferred regulatory region (I)
CC comprising nucleotide sequences essential for initiating transcription
CC of the Ms45 gene. A method of mediating male fertility in a plant is
CC provided that involves introducing an expression vector comprising a
CC promoter operably linked to (I) into a plant where the exogenous gene
CC impacts male fertility of the plant and (I) controls expression of the
CC exogenous gene. A method of producing hybrid seeds is also provided.
CC Sequences AAH76341-355 represent a series of 5' deletions in the Ms45
CC promoter region, used for determining the essential region of Ms45
CC promoter.
XX
SQ Sequence 10 BP; 0 A; 5 C; 5 G; 0 U; 0 other;
XX
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCCGGGCC 9
DB 1 GGCCGGGCC 9
RESULT 257
AAH19876/c
ID AAS19876 standard; DNA; 10 BP.
XX
AC AAS19876;
XX
DT 08-MAY-2002 (first entry)
XX
DE Oligonucleotide #56 to detect human RANGAP1 gene polymorphisms.
XX
KM Human; single nucleotide polymorphism; SNP: RANGAP1; haplotyping
XX chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
XX cancer; irregular cell cycle associated disorder; primer; ss.
XX
OS Homo sapiens.
XX
PN W0200179240-A2.
XX
PD 25-OCT-2001.
XX
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```
PF 17-APR-2001; 2001MO-US12455.
XX
PR 17-APR-2000; 2000US-198072P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshy B;
XX WPI; 2002-075068/10.
XX
PT Genotyping human Ran GTPase activating protein 1 gene of individual for
PT determining haplotype of individual, involves determining identity of
PT nucleotide pair at specific polymorphic sites for two copies of the
XX gene -
XX
PS Claim 17; Page 16; 148pp; English.
XX
CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC genotyping the RANGAP1 gene. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC primer-extension oligonucleotides for detecting the RANGAP1 gene
CC polymorphisms. The polymorphisms and screened compounds are useful for
CC treatment of diseases associated with RANGAP1 activity, such as
CC cancer and other disorders associated with an irregular cell cycle.
CC AAS19821-AAS19898 represent primer-extension oligonucleotides for
XX detecting human RANGAP1 gene polymorphisms.
XX
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 U; 0 other;
XX
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCCGGGCC 9
DB 9 GTCCCTGGCC 1
RESULT 258
AAH64374
ID AAH64374 standard; cDNA; 10 BP.
XX
AC AAH64374;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1214.
XX
KM Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN W0200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000MO-US31922.
XX
PR 24-NOV-1999; 99US-0448480.
XX
PA (UYUO) UNIV JOHNS HOPKINS.
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
PT New isolated polymorphisms, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
```

PS Claim 13; Page 67; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;
QY Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 GCCAGGCCA 9
QY 7 GCCAGGCCA 15
DB 1 GCCAGGCCA 9
RESULT 259
AAH64375
ID AAH64375 standard; cDNA; 10 BP.
XX AAH64375;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1215.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
XX
XX MO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000MO-US31922.
XX
XX 24-NOV-1999; 99US-0448480.
XX
XX PA (UYUO) UNITV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell
XX type, such as cancer cell, comprises transcriptomes expressed in
XX particular cell types -
XX
XX
XX Claim 13; Page 67; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences
XX AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
XX in the invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of
XX the transcriptomes described in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;
QY Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 GCCAGGCCA 15

DB 1 GCCAGGCCA 9
RESULT 260
AAH32856
ID AAH32856 standard; cDNA; 10 BP.
XX
XX AAH32856;
XX
XX 13-AUG-2001 (first entry)
XX
XX LPS activated human monocyte expression gene cDNA tag SEQ.229.
XX
XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
XX expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
XX Homo sapiens.
XX
XX JP2001069993-A.
XX
XX 21-MAR-2001.
XX
XX 28-APR-2000; 2000JP-0131079.
XX
XX 08-JUL-1999; 99JP-0195103.
XX
XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX
XX WPI; 2001-304369/32.
XX
XX LPS activated human monocyte expression gene group -
XX
XX
XX Claim 19; Page 39; 52pp; Japanese.
XX
XX The present invention describes an lipopolysaccharide (LPS) activated
XX human monocyte expression gene group consisting of the high-ranking 50
XX genes of the highest expression among the genes expressed by human
XX monocyte stimulated by LPS in which the cDNA of each gene has the base
XX sequence of (AAH32628 to AAH32677) continuous to the base sequence
XX 5'-CATG-3' nearest to the polyA region. The gene group is useful for the
XX development of new means for the diagnosis and the treatment of various
XX human diseases in which human monocyte plays an important role.
XX AAH32628 to AAH32943 represent specifically claimed LPS activated human
XX monocyte expression gene cDNA tags from the present invention. AAH32944
XX represents an LPS activated human monocyte expression gene cDNA sequence
XX encoding AAB98009, which are given in the exemplification of the present
XX invention.
XX
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;
QY Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 GCCAGGCCA 15
QY 7 GCCAGGCCA 15
DB 1 GCCAGGCCA 9
RESULT 261
ABK95840/C
ID ABK95840 standard; DNA; 10 BP.
XX
XX ABK95840;
XX
XX 24-SEP-2002 (first entry)
XX
XX Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #11.
XX
XX Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
XX glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
XX amino acid transporter disorder; single nucleotide polymorphism; SNP.

```

XX OS Homo sapiens.
XX PN WO200244198-A2.
XX PD 06-JUN-2002.
XX PF 29-NOV-2001; 2001WO-US44781.
XX PR 30-NOV-2000; 2000US-250254P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Bieglecki KM, Kazemi A, Russo DP, Sausker EA;
XX WPI; 2002-519580/55.
XX PT Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
XX PT Amino Acid Transporter), Member 4 isogenes, for improving efficiency
XX PT and reliability in drug development for treating cancers -
XX PS Claim 17; Page 16; 139pp; English.
XX CC The invention relates to an isolated polynucleotide (I) comprising a
XX CC first nucleotide sequence which comprises solute carrier family 1
XX CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes
XX CC (II) and an isolated polypeptide (III) comprising an amino acid sequence
XX CC which is a polymorphic variant of a reference sequence for SLC1A4
XX CC protein. Also described are methods for: (1) haplotyping or genotyping
XX CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
XX CC gene of an individual; (3) identifying an association between a trait and
XX CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) is useful
XX CC in screening for drugs targeting (III) that are useful for treating
XX CC cancer, neurological diseases and amino acid transporter disorders. The
XX CC methods are useful for improving the efficiency and reliability of
XX CC several steps in the discovery and development of drugs for treating
XX CC diseases associated with SLC1A4 activity. The haplotyping method is also
XX CC used by the pharmaceutical research scientist to validate SLC1A4 as a
XX CC candidate target for treating a specific condition or disease predicted
XX CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
XX CC and amino acid transporter disorders, and in the design of clinical
XX CC trials for treating a specific condition of disease associated with
XX CC SLC1A4 activity. The methods are also useful for screening compounds
XX CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,
XX CC prognostic and therapeutic methods. ABK95761-ABK95877 represent
XX CC SLC1A4 gene allele-specific oligonucleotides, primer extension
XX CC oligonucleotides and related PCR primers used to identify single
XX CC nucleotide polymorphisms (SNP) of the gene.
XX SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 U; 0 other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGCCGAGGC 13
   |||||
   |||||
Db 10 GGCCCTGGC 2

RESULT 262
ABV65097/C
ID ABV65097 standard; cDNA; 11 BP.
XX ABV65097;
XX AC
XX XX 21-OCT-2002 (first entry)
XX DT
XX XX Human skin EST 2883.
XX DE
XX XX Human; skin; dermatological; vulnery; antipsoriatic; antisephorhaeic;
XX KM immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

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XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP15179.
XX PR 03-JAN-2001; 2001DE-1000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer -
XX PS Disclosure; Page 105; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention.
XX SQ Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 other;

Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCGAGCCA 15
   |||||
   |||||
Db 10 GCCTGGCCA 2

RESULT 263
ABV69411
ID ABV69411 standard; cDNA; 11 BP.
XX ABV69411;
XX AC
XX XX 21-OCT-2002 (first entry)
XX DT
XX XX Human skin EST 7197.
XX DE
XX XX Human; skin; dermatological; vulnery; antipsoriatic; antisephorhaeic;
XX KM immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP15179.
XX PR 03-JAN-2001; 2001DE-1000127.
XX PA (HENK ) HENKEL KGAA.
XX XX

```


PI Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 CC homeostasis and identifying cosmetic or pharmaceutical agents against
 CC e.g. skin cancer -
 XX
 PS Disclosure; Page 226; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.
 CC
 XX
 SQ Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 other;
 XX
 Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Qy 5 GGGCCAGGC 13
 |||||
 Db 2 GGGCTGGC 10
 XX
 RESULT 264
 ID AAA82879 standard; DNA; 19 BP.
 XX
 AC AAA82879;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE cdk4 ribozyme binding site #60.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 KW restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO200032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US28772.
 XX
 PR 04-DEC-1998; 98US-0110954.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 XX WPI; 2000-412314/35.
 XX
 PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 CC RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1 -
 XX
 PS Disclosure; Page 53; 109pp; English.
 XX
 CC The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in

CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 XX
 SQ Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;
 XX
 Query Match 37.0%; Score 7.4; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Qy 6 GGGCCAGGC 14
 |||||
 Db 11 GGGCTGGC 19
 XX
 RESULT 265
 ID AAH58041 standard; DNA; 19 BP.
 XX
 AC AAH58041;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:465.
 XX
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytosolic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; vitruide;
 KW antisticking; ophthalmological; keratolytic; gene therapy; vital wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-US29500.
 XX
 PR 26-OCT-1999; 99US-0161532.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Robbins JM, Tritz R;
 XX
 XX WPI; 2001-300427/31.
 XX
 PT Treating proliferative skin or eye diseases and scarring, using
 PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -
 XX
 PS Example 1; Page 105; 408pp; English.
 XX
 CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytosolic, antiseborrheic, antidiabetic, antisticking,
 CC ophthalmological, vulnery, keratolytic and vitruide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AA457577 to AA462099 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;
Query Match 37.0%; Score 7.4; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 GGCCAGGCC 14
Db 11 GGCCAGGCC 19
RESULT 266
AAT09655/c
ID AAT09655 standard; DNA; 8 BP.
XX
AC AAT09655;
XX
DT 25-MAR-2003 (updated)
DT 25-JUN-1996 (first entry)
XX
DE 3'-primer used for characterisation of human biological samples.
XX
KW 3'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN WO531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US06032.
XX
PR 16-MAY-1994; 94US-0242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznielo CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers
PT used for genome mapping and disease diagnosis
XX
PS Disclosure; Page 19; 72pp; English.
XX
SQ The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC target human protein coding regions, together comprise a PCR primer
CC kit with 1361 possible primer pairs. The kit is used in a new method
CC for the characterisation of nucleic acid sequences obtd. from human
CC biological samples, which comprises PCR amplification and indexing of
CC the prods. w.r.t the primer pair that hybridised to its delineating
CC subsequences. The method may be used in the identification, cloning
CC and analysis of genes, e.g. in genome mapping, and disease
CC diagnosis.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 8 BP; 0 A; 3 C; 2 G; 3 T; 0 other;
Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 AGGCCAA 16
Db 7 AGGCCAA 1
RESULT 267
AAT09656/c
ID AAT09656 standard; DNA; 8 BP.
XX
AC AAT09656;
XX
DT 25-MAR-2003 (updated)
DT 25-JUN-1996 (first entry)
XX
DE 3'-primer used for characterisation of human biological samples.
XX
KW 3'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN WO531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US06032.
XX
PR 16-MAY-1994; 94US-0242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznielo CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers
PT used for genome mapping and disease diagnosis
XX
PS Disclosure; Page 19; 72pp; English.
XX
SQ The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC target human protein coding regions, together comprise a PCR primer
CC kit with 1361 possible primer pairs. The kit is used in a new method
CC for the characterisation of nucleic acid sequences obtd. from human
CC biological samples, which comprises PCR amplification and indexing of
CC the prods. w.r.t the primer pair that hybridised to its delineating
CC subsequences. The method may be used in the identification, cloning
CC and analysis of genes, e.g. in genome mapping, and disease
CC diagnosis.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 8 BP; 0 A; 2 C; 2 G; 4 T; 0 other;
Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 AGGCCAA 16
Db 7 AGGCCAA 1
RESULT 268
AAT09366
ID AAT09366 standard; DNA; 8 BP.
XX
AC AAT09366;
XX
DT 25-MAR-2003 (updated)

DT	21-JUN-1996	(first entry)	
XX			
DE	5'-primer used for characterisation of human biological samples.		
XX			
KW	5'-primer; human; protein coding region; PCR primer kit;		
KW	characterisation; biological samples; PCR amplification; indexing;		
KW	identification; cloning; analysis; genes; genome mapping;		
KW	disease diagnosis; ss.		
XX			
OS	Synthetic.		
XX			
PN	W09531574-A1.		
XX			
PD	23-NOV-1995.		
XX			
PF	12-MAY-1995; 95WO-US06032.		
XX			
PR	16-MAY-1994; 94US-024287.		
XX			
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.		
XX			
P1	Lopeznielo CE, Nigam SK;		
XX			
DR	WPI: 1996-010958/01.		
XX			
PT	Characterisation of nucleotide sequences using primer pairs - by PCR		
XX	amplification and indexing of amplification prods. w.r.t. primers		
PT	used for genome mapping and disease diagnosis		
XX			
PS	Claim 5; Page 44; 72pp; English.		
XX			
CC	The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which		
CC	target human protein coding regions, together comprise a PCR primer		
CC	kit with 1361 possible primer pairs. The kit is used in a new method		
CC	for the characterisation of nucleic acid sequences obtd. from human		
CC	biological samples, which comprises PCR amplification and indexing of		
CC	the prods. w.r.t. the primer pair that hybridised to its delineating		
CC	subsequences. The method may be used in the identification, cloning		
CC	and analysis of genes, e.g. in genome mapping, and disease		
CC	diagnosis.		
XX	(Updated on 25-MAR-2003 to correct PI field.)		
SQ	Sequence 8 BP; 4 A; 2 C; 2 G; 0 U; 0 other;		
	Query Match	35.0%; Score 7; DB 1; Length 8;	
	Best Local Similarity	100.0%; Pred. No. 5.8e+02;	
	Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	10 AGGCCAA 16		
Db	2 AGGCCAA 8		
RESULT 269			
AAT09389			
ID	AAT09389 standard; DNA; 8 BP.		
XX			
AC	AAT09389;		
XX			
DT	25-MAR-2003 (updated)		
DT	21-JUN-1996 (first entry)		
XX			
DE	5'-primer used for characterisation of human biological samples.		
XX			
KW	5'-primer; human; protein coding region; PCR primer kit;		
KW	characterisation; biological samples; PCR amplification; indexing;		
KW	identification; cloning; analysis; genes; genome mapping;		
KW	disease diagnosis; ss.		
XX			
OS	Synthetic.		
XX			
PN	W09531574-A1.		
XX			

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PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US06032.
XX
PR 16-MAY-1994; 94US-0242887.
XX
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers
PS used for genome mapping and disease diagnosis
PS Claim 5; Page 44; 72pp; English.
XX
CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC target human protein coding regions, together comprise a PCR primer
CC kit with 1361 possible primer pairs. The kit is used in a new method
CC for the characterisation of nucleic acid sequences obtd. from human
CC biological samples, which comprises PCR amplification and indexing of
CC the prods. w.r.t the primer pair that hybridised to its delineating
CC subsequences. The method may be used in the identification, cloning
CC and analysis of genes, e.g. in genome mapping, and disease
CC diagnosis.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 8 BP; 3 A; 2 C; 3 G; 0 U; 0 other;
Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 AGGCCAA 16
|||
|||
|||
DB 1 AGGCCAA 7
RESULT 270
AAT09459
ID AAT09459 standard; DNA; 8 BP.
XX
AC AAT09459;
XX
DT 25-MAR-2003 (updated)
XX 21-JUN-1996 (first entry)
DE 5'-primer used for characterisation of human biological samples.
XX
KW 5'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN W09531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US06032.
XX
PR 16-MAY-1994; 94US-0242887.
XX
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR

```

PT amplification and indexing of amplification prods. w.r.t. primers
 PT used for genome mapping and disease diagnosis
 XX
 PS Claim 5; Page 44; 72pp; English.
 CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
 CC target human protein coding regions, together comprise a PCR primer
 CC kit with 1361 possible primer pairs. The kit is used in a new method
 CC for the characterisation of nucleic acid sequences obtd. from human
 CC biological samples, which comprises PCR amplification and indexing of
 CC the prods. w.r.t. the primer pair that hybridised to its delineating
 CC subsequences. The method may be used in the identification, cloning
 CC and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 SQ Sequence 8 BP; 3 A; 2 C; 3 G; 0 U; 0 other;
 Query Match 35.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 AGGCCAA 16
 Db 2 AGGCCAA 8
 RESULT 271
 AAT09572/c
 ID AAT09572 standard; DNA; 8 BP.
 XX
 AC AAT09572;
 XX
 DT 25-MAR-2003 (updated)
 DT 25-JUN-1996 (first entry)
 XX
 DE 3'-primer used for characterisation of human biological samples.
 XX
 KM 3'-primer; human; protein coding region; PCR primer kit;
 KM characterisation; biological samples; PCR amplification; indexing;
 KM identification; cloning; analysis; genes; genome mapping;
 KM disease diagnosis; ss.
 XX
 OS Synthetic.
 OS
 PN MO9531574-A1.
 XX
 PD 23-NOV-1995.
 XX
 PF 12-MAY-1995; 95WO-US06032.
 XX
 PR 16-MAY-1994; 94US-0242887.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Lopeznielo CE, Nigam SK;
 XX
 DR WPI; 1996-010958/01.
 XX
 PT Characterisation of nucleotide sequences using primer pairs - by PCR
 PT amplification and indexing of amplification prods. w.r.t. primers
 PT used for genome mapping and disease diagnosis
 XX
 PS Disclosure; Page 19; 72pp; English.
 CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
 CC target human protein coding regions, together comprise a PCR primer
 CC kit with 1361 possible primer pairs. The kit is used in a new method
 CC for the characterisation of nucleic acid sequences obtd. from human
 CC biological samples, which comprises PCR amplification and indexing of
 CC the prods. w.r.t. the primer pair that hybridised to its delineating
 CC subsequences. The method may be used in the identification, cloning
 CC and analysis of genes, e.g. in genome mapping, and disease

CC diagnosis.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 8 BP; 0 A; 3 C; 2 G; 3 T; 0 other;
 Query Match 35.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 AGGCCAA 16
 Db 8 AGGCCAA 2
 RESULT 272
 AAX29560/c
 ID AAX29560 standard; DNA; 8 BP.
 XX
 AC AAX29560;
 XX
 DT 03-JUN-1999 (first entry)
 XX
 DE Primer for human G-protein coupled receptor genes.
 XX
 KM Nucleic acid amplification; nuclear receptor; G-protein coupled receptor;
 KM apoptosis; DNA repair; DNA replication; plant biology; agriculture;
 KM human; veterinary medicine; reproduction; microbiology; hybridisation;
 KM environmental science; DNA fingerprinting; PCR primer; ss.
 XX
 OS Synthetic.
 OS
 OS Homo sapiens.
 OS
 PN MO9911823-A2.
 XX
 PD 11-MAR-1999.
 XX
 PF 04-SEP-1998; 98WO-US18392.
 XX
 PR 05-SEP-1997; 97US-0925816.
 XX
 PA (KIMM-) KIMMEL CANCER CENT SYDNEY.
 XX
 PI McClelland M, Pesole G;
 XX
 DR WPI; 1999-205200/17.
 XX
 PT Subset of primers able to amplify group of related sequences
 PT
 PS Claim 21; Page 75; 92pp; English.
 XX
 CC The invention provides primers (AAX29501-X29679) for identifying
 CC sequences encoding structurally or functionally related proteins such as
 CC nuclear or G-protein coupled receptors, apoptosis-related or DNA
 CC repair/replication proteins. The identified sequences are broadly useful
 CC in plant biology, agriculture, human or veterinary medicine,
 CC reproduction, microbiology or environmental science, e.g. to study
 CC expression of nuclear receptors at different stages of tissue development
 CC or after treatment with particular drugs. It is also used for DNA
 CC fingerprinting (to generate products useful for differential
 CC hybridisation), or, where a 3'-anchor primer is used, to isolate the
 CC 3'-ends of mRNA sequences. Sequences AAX29526-X29583 represent claimed
 CC primers specific for human G-protein coupled receptor genes.
 CC
 SQ Sequence 8 BP; 0 A; 4 C; 2 G; 2 T; 0 other;
 Query Match 35.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 GGCCACG 12
 Db 8 GGCCACG 2

```

RESULT 273
AAK29558/C
ID AAK29558 standard; DNA; 8 BP.
XX
XX AAK29558;
AC
DT 03-JUN-1999 (first entry)
XX
XX
DE Primer for human G-protein coupled receptor genes.
XX
XX Nucleic acid amplification; nuclear receptor; G-protein coupled receptor;
XX apoptosis; DNA repair; DNA replication; plant biology; agriculture;
XX human; veterinary medicine; reproduction; microbiology; hybridisation;
XX environmental science; DNA fingerprinting; PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX MO9911823-A2.
XX
XX 11-MAR-1999.
PD
XX
XX 04-SEP-1998; 98WO-US18392.
XX
XX 05-SEP-1997; 97US-0925816.
XX
XX (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
XX McClelland M, Pesole G;
XX
XX WPI; 1999-205200/17.
XX
XX
XX Subset of primers able to amplify group of related sequences
XX
XX Claim 21; Page 75; 92pp; English.
XX
XX
XX The invention provides primers (AAK295501-X29679) for identifying
XX sequences encoding structurally or functionally related proteins such as
XX nuclear or G-protein coupled receptors, apoptosis-related or DNA
XX repair/replication proteins. The identified sequences are broadly useful
XX in plant biology, agriculture, human or veterinary medicine,
XX reproduction, microbiology or environmental science, e.g. to study
XX expression of nuclear receptors at different stages of tissue development
XX or after treatment with particular drugs. It is also used for DNA
XX fingerprinting (to generate products useful for differential
XX hybridisation), or, where a 3'-anchor primer is used, to isolate the
XX 3'-ends of mRNA sequences. Sequences AAK29526-X29583 represent claimed
XX primers specific for human G-protein coupled receptor genes.
XX
XX Sequence 8 BP; 0 A; 4 C; 2 G; 2 T; 0 other;
XX
XX
XX Query Match 35.0%; Score 7; DB 1; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 5.8e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6 GGCGAGG 12
XX |||||
XX 7 GGCGAGG 1
XX
XX
RESULT 274
AAK80793
ID AAK80793 standard; DNA; 8 BP.
XX
XX AAK80793;
AC
XX
XX 24-NOV-2000 (first entry)
DT
XX
XX A. thaliana primer walking octamer SRO ID NO: 106.
DE
XX
XX Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX

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OS Arabidopsis thaliana.
XX
XX US6083695-A.
XX
XX 04-JUL-2000.
XX
XX 21-MAY-1997; 97US-0859954.
XX
XX 15-APR-1996; 96US-0632782.
XX
XX (UYHO-) UNIV HOUSTON.
XX (HARD/) HARDIN S H.
XX
XX Hardin PE, Hardin SH, Homayouni R;
XX
XX WPI; 2000-474852/41.
XX
XX Sequencing an unknown DNA molecule for the polymerase chain reaction
XX and other primer processes comprises primer walking of octamer
XX oligonucleotides
XX
XX Example 8: Column 77-78; 161pp; English.
XX
XX This invention describes a novel method for sequencing an unknown DNA
XX molecule which comprises selecting a library primer from an octamer
XX oligonucleotide library consisting of 48 8-bp sequences and
XX corresponding complementary sequences, where the library primer is
XX complementary to a known sequence adjacent to the unknown sequence or
XX is complementary to a sequence in a known extension product. The method
XX is useful for DNA nucleotide sequencing, in PCR, and in other processes
XX which make use of primers. The octamers are used to identify coding
XX sequences. Primer walking using the octamer libraries is advantageous
XX over other sequencing methods because it does not require multiple
XX cloning steps nor subsequent template preparations, and it is a
XX directed and methodical approach. ABA80688-A81253 represent the octamer
XX primers used in the primer walking method of the invention.
XX
XX Sequence 8 BP; 4 A; 2 C; 2 G; 0 U; 0 other;
XX
XX Query Match 35.0%; Score 7; DB 1; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 5 8e+02;
XX Matches 7; Conservative 0; Mismatches -0; Indels 0; Gaps 0.
XX
XX QY 12 GCCAAG 18
XX |||||
XX 1 GCCAAG 7
XX
XX Db
XX
XX RESULT 275
XX AAA81046
XX ID AAA81046 standard; DNA; 8 BP.
XX
XX AAA81046;
XX
XX 24-NOV-2000 (first entry)
XX
XX A. thaliana primer walking octamer SEQ ID NO: 359.
XX
XX Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
XX Arabidopsis thaliana.
XX
XX US6083695-A.
XX
XX 04-JUL-2000.
XX
XX 21-MAY-1997; 97US-0859954.
XX
XX 15-APR-1996; 96US-0632782.
XX
XX (UYHO-) UNIV HOUSTON.
XX (HARD/) HARDIN S H.
XX
XX

```

PI Hardin PE, Hardin SH, Homayouni R;
 XX WPI; 2000-474852/41.
 XX
 PT Sequencing an unknown DNA molecule for the polymerase chain reaction
 PT and other primer processes comprises primer walking of octamer
 PT oligonucleotides -
 XX
 XX Example 8; Column 205-206; 161pp; English.
 CC This invention describes a novel method for sequencing an unknown DNA
 CC molecule which comprises selecting a library primer from an octamer
 CC oligonucleotide library consisting of 48 8-bp sequences and
 CC corresponding complementary sequences, where the library primer is
 CC complementary to a known sequence adjacent to the unknown sequence or
 CC is complementary to a sequence in a known extension product. The method
 CC is useful for DNA nucleotide sequencing, in PCR, and in other processes
 CC which make use of primers. The octamers are used to identify coding
 CC sequences. Primer walking using the octamer libraries is advantageous
 CC over other sequencing methods because it does not require multiple
 CC cloning steps nor subsequent template preparations, and it is a
 CC directed and methodical approach. AAA80688-A81253 represent the octamer
 CC primers used in the primer walking method of the invention.
 CC
 SQ Sequence 8 BP; 3 A; 3 C; 1 G; 1 T; 0 other;
 XX
 Query Match 35.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 13 CCAAGT 19
 Db 2 CCAAGT 8
 XX
 RESULT 276
 AAD2387/c
 ID AAD22387 standard; DNA; 8 BP.
 XX
 AC AAD22387;
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Oligonucleotide #1 to generate fatty acid biosynthesis gene construct.
 XX
 KM Cotton; delta9-desaturase; fatty acid delta12-desaturase; palmitic acid;
 KM linoleic acid; stearic acid; oleic acid; transgenic plant;
 KM cotton seed oil; ss.
 XX
 OS Unidentified.
 XX
 PN WO200179499-A1.
 XX
 PD 25-OCT-2001.
 XX
 PF 18-APR-2001; 2001WO-AU00436.
 XX
 PR 18-APR-2000; 2000US-198124P.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Green A, Singh S, Liu Q;
 XX
 DR WPI; 2001-602932/68.
 XX
 PT Modifying endogenous oil of cotton plants, to produce cotton seed oil
 PT with reduced palmitic and/or linoleic acid content, involves producing
 PT transgenic plants containing a fatty acid biosynthesis gene in a
 PT construct -
 XX
 PS Example 11; Page 90; 201pp; English.
 XX
 CC The invention relates to a method for modifying the endogenous oil of a

CC cotton plant, to produce cotton seed oil. The method comprises producing
 CC a transgenic cotton plant having a gene construct which includes a fatty
 CC acid biosynthesis gene operably linked to a promoter sequence capable of
 CC conferring expression of the delta9-desaturase (delta9 stearyl-ACP
 CC desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-
 CC desaturase) gene in the seed of a cotton plant. The invention is useful
 CC for producing cottonseed oil with reduced palmitic and/or linoleic acid
 CC content, and increased stearic and/or oleic acid content. The present
 CC DNA sequence is an oligonucleotide which is used for generating fatty
 CC acid biosynthesis gene construct related to the invention.
 CC
 SQ Sequence 8 BP; 0 A; 3 C; 5 G; 0 U; 0 other;
 XX
 Query Match 35.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 3 CCGGCCC 9
 Db 7 CCGGCCC 1
 XX
 RESULT 277
 AAF20849/c
 ID AAF20849 standard; DNA; 9 BP.
 XX
 AC AAF20849;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human adenosine A1 receptor polynucleotide fragment #2416.
 XX
 KM Low adenosine oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KM surfactant hypoproduction; pulmonary obstruction; impeded respiration;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI (NYCE/) NYCE J W.
 XX
 DR NYCE JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Claim 14; Page 106; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with

CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC condition selected from pulmonary vasoconstriction, inflammation, or
CC allergies, asthma, impaired respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAPI8434 to AAPI21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.

XX
SQ Sequence 9 BP; 0 A; 3 C; 5 G; 1 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+02; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0;

OY 8 CCAGGCC 14
Db 9 CCAGGCC 3

RESULT 278
AAA34727/c
ID AAA34727 standard; DNA; 9 BP.

XX
AC AAA34727;

XX
DT 28-JUL-2000 (first entry)

XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2416.

KM Human; adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphorothioate; impaired respiration; inflammation; allergy;
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KM antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KM lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM cancer; leukemia; lymphoma; carcinoma; metastasis; ss.

XX
OS Homo sapiens.

XX
PN MO200009525-A2.

XX
PD 24-FEB-2000.

XX
PF 03-AUG-1999; 99WO-US17712.

XX
PR 03-AUG-1998; 98US-0095212.

XX
PA (UYEC-) UNIV EAST CAROLINA.

XX
PI NYce JW;

XX
DR WPI; 2000-205971/18.

XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers

XX
PS Disclosure; Page 571; 1343pp; English.

XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32333 to AAA3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA33323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

XX
SQ Sequence 9 BP; 0 A; 3 C; 5 G; 1 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+02; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0;

OY 8 CCAGGCC 14
Db 9 CCAGGCC 3

RESULT 279
ABQ72098/c
ID ABQ72098 standard; DNA; 9 BP.

XX
AC ABQ72098;

XX
DT 28-AUG-2002 (first entry)

XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2396.

XX
KM Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX
OS Homo sapiens.

XX
OS Synthetic.

XX
PN MO200242459-A2.

XX
PD 30-MAY-2002.

XX
PF 20-NOV-2001; 2001WO-US43438.

XX
PR 20-NOV-2000; 2000US-0716637.

XX
PA (SANG-) SANGAMO BIOSCIENCES INC.

XX
PI Liu Q;

XX
DR WPI; 2002-500284/53.

XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus

Example 1, Page 61, 81pp; English.

The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3',-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (1) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the phenotypic and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.

Sequence 9 BP, 1 A, 2 C, 3 G, 3 T, 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

12 GCCAAG 18
|||||
8 GCCAAG 2

RESULT 280
ABQ72099/C
ID ABQ72099 standard; DNA; 9 BP.
XX
XX ABQ72099;
XX
XX 28-AUG-2002 (first entry).
XX DE Zinc finger protein related oligonucleotide target SEQ ID NO:2397.
XX
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX W0200242459-A2.
XX
XX 30-MAY-2002.
XX
XX 20-NOV-2001; 2001WO-US43438.
XX PF
XX 20-NOV-2000; 2000US-0716637.
XX PR
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX PA
XX L1u Q;
XX
XX WPI; 2002-500284/53.
XX
XX
XX New zinc finger protein that binds to target site, useful in studying
XX gene function and for human therapeutics and plant engineering,
XX comprises first, second and third zinc fingers, ordered from N- to
XX C-terminus -
XX
XX Example 1, Page 61, 81pp; English.
XX

CC	The present invention describes a zinc finger protein (I) that binds to
CC	a target site, comprising a first (F1), a second (F2), and a third (F3)
CC	zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC	target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC	and a third (S3) target substrate. Also described are: (1) a polypeptide
CC	(II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC	(3) designing (IV) (I) involves selecting the F1 zinc finger such that
CC	it binds to the S1 target substrate, selecting the F2 zinc finger such
CC	that it binds to the S2 target substrate, and selecting the F3 zinc
CC	finger such that it binds to the S3 target substrate, thus designing (I)
CC	that binds to a target site. (I) is useful for recognition of triplet
CC	target substrates having the nucleotide G in the 5'-most position of the
CC	substrate. (I) is useful in studying gene function, and for human
CC	therapeutics and plant engineering. (I), (II) or (III) is useful in
CC	therapeutic methods to modulate the expression of a target region within
CC	a subject, in diagnostic methods for sequence specific detection of
CC	target nucleic acid in a sample, and in assays to determine the
CC	phenotype and function of gene expression. (I) has improved affinity
CC	and specificity for their target sequences, as well as enhanced
CC	biological activity. ABQ72123 to ABQ72214 and ABRP8191 to APP51230
CC	represent DNA target sequences and zinc finger peptides which are given
CC	in the exemplification of the present invention.
SQ	Sequence 9 BP; 1 A; 2 C; 3 G; 3 T; 0 other;
Query Match	35.0%; Score 7; DB 1; Length 9;
Best Local Similarity	100.0%; Pred. No. 5.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
OY	12 GCCAAG 18 8 GCCAAG 2
Dd	
RESULT 281	
ABK95837/c	
ID	ABK95837 standard; DNA; 10 BP.
XX	
AC	ABK95837;
XX	
DT	24-SEP-2002 (first entry)
XX	
DE	Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #8.
XX	
KW	Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer; glutamate/neutral amino acid transporter; neurological disease; PCR; ss; amino acid transporter disorder; single nucleotide polymorphism; SNP.
XX	
OS	Homo sapiens.
XX	
PN	WO200244198-A2.
XX	
PD	06-JUN-2002.
XX	
PF	29-NOV-2001; 2001WO-US44781.
XX	
PR	30-NOV-2000; 2000US-250254P.
XX	
PA	(GENA-) GENAISANCE PHARM INC.
XX	
PI	Bieglecki KM, Kazemi A, Russo DP, Sausker EA;
XX	
DR	WP1; 2002-519580/55.
XX	
PT	Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral Amino Acid Transporter), Member 4 isogenes, for improving efficiency and reliability in drug development for treating cancers -
FT	
XX	
PS	Claim 17; Page 16; 139pp; English.
XX	
CC	The invention relates to an isolated polynucleotide (I) comprising a
CC	first nucleotide sequence which comprises solute carrier family 1
CC	(glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes

CC (II) and an isolated polypeptide (III) comprising an amino acid sequence
 CC which is a polymorphic variant of a reference sequence for SLClA4
 CC protein. Also described are methods for: (1) haplotyping or genotyping
 CC SLClA4 gene of an individual; (2) predicting a haplotype pair for SLClA4
 CC gene of an individual; (3) identifying an association between a trait and
 CC at least one haplotype or haplotype pair of SLClA4 gene. (III) is useful
 CC in screening for drugs targeting (III) that are useful for treating
 CC cancer, neurological diseases and amino acid transporter disorders. The
 CC methods are useful for improving the efficiency and reliability of
 CC several steps in the discovery and development of drugs for treating
 CC diseases associated with SLClA4 activity. The haplotyping method is also
 CC used by the pharmaceutical research scientist to validate SLClA4 as a
 CC candidate target for treating a specific condition or disease predicted
 CC to be associated with SLClA4 activity, e.g. cancer, neurological diseases
 CC and amino acid transporter disorders, and in the design of clinical
 CC trials for treating a specific condition of disease associated with
 CC SLClA4 activity. The methods are also useful for screening compounds
 CC targeting SLClA4. Anti-SLClA4 antibody is useful in diagnostic,
 CC prognostic and therapeutic methods. ABK95761-ABK95877 represent
 CC SLClA4 gene allele-specific oligonucleotides, primer extension
 CC oligonucleotides and related PCR primers used to identify single
 CC nucleotide polymorphisms (SNP) of the gene.

XX
 SQ Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 other;
 Query Match 35.0%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGAGGCC 14
 |||||
 10 CCGAGGCC 4

Db
 RESULT 282
 ABV63037/c
 ID ABV63037 standard; cDNA; 11 BP.
 XX
 AC ABV63037;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 823.
 XX
 DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP15179.
 XX
 PR 03-JAN-2001; 2001DE-1000127.
 XX
 PA (HENK) HENKEL KGAA.
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer
 XX
 PS Disclosure; Page 48; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)

CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.

XX
 SQ Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;
 Query Match 35.0%; Score 7; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGG 12
 |||||
 7 GGCCAGG 1

Db
 RESULT 283
 ABV70458/c
 ID ABV70458 standard; cDNA; 11 BP.
 XX
 AC ABV70458;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 8244.
 XX
 DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP15179.
 XX
 PR 03-JAN-2001; 2001DE-1000127.
 XX
 PA (HENK) HENKEL KGAA.
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer
 XX
 PS Claim 24; Page 264; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.

XX
 SQ Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 other;
 Query Match 35.0%; Score 7; DB 1; Length 11;

PF 02-JUL-1998; 98WO-US13903.
 XX
 PR 02-JUL-1997; 97US-0051573.
 XX
 PA (GENZ) GENZYME CORP.
 XX
 PI Beaudry GA, Bertelsen AH, Galella EA, Madden SL;
 XX WPI; 1999-106079/09.
 DR
 PT Diagnosis of cancer in potentially neoplastic samples - by comparing
 PT the level of transcription between RNA transcripts in two tissue
 PT samples, useful for providing an extensive profile of gene
 PT expression in rat embryo fibroblast (REF) cells
 XX
 PS Example 2; Page 15; 32pp; English.
 XX
 CC A method has been developed for the diagnosis of cancer in potentially
 CC neoplastic samples. The method comprises comparing the level of
 CC transcription between RNA transcripts in two tissue samples (which are
 CC of the same type), where the first sample is potentially neoplastic, and
 CC the second sample is normal human tissue. The first sample is
 CC categorized as neoplastic if its level of transcription is lower than
 CC that of the second sample. The transcript is selected from Alu, RAS,
 CC U6 snRNA, 16S RNA, EGR-1, ribosomal protein S27, ETS-1, 28S RNA, CGR11,
 CC and LIMK-2, and it is identified by a tag selected from ribosomal
 CC protein L13a, alpha-tubulin (T1) and (T2), thymosin beta-4, and gamma-
 CC actin. The present sequence represents a serial analysis of gene
 CC expression (SAGE) tag from the present invention. The use of SAGE tags
 CC provides an extensive profile of gene expression in rat embryo
 CC fibroblast (REF) cells containing the (non)-functional p53 tumour
 CC suppression gene. The discovery of new SAGE tags, which are regulated
 CC by p53, enables the diagnosis of genes that are related to cell cycle
 CC control and tumorigenesis.
 CC
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;
 XX
 Query Match 34.0%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 6 GGCCAGGCCA 15
 |||||
 Db 1 GGCTTGGCTA 10
 RESULT 287
 AAZ79322
 ID AAZ79322 standard; DNA; 10 BP.
 XX
 AC AAZ79322;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:1750.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO965924-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US13800.
 XX
 PR 19-JUN-1998; 98US-0089833.
 PR 19-JUN-1998; 98US-0089844.
 PR 19-JUN-1998; 98US-0089853.
 PR 19-JUN-1998; 98US-0089878.

PR 19-JUN-1998; 98US-0089991.
 PR 19-JUN-1998; 98US-0089992.
 PR 19-JUN-1998; 98US-0089993.
 PR 19-JUN-1998; 98US-0089994.
 PR 19-JUN-1998; 98US-0089997.
 PR 19-JUN-1998; 98US-0089999.
 PR 19-JUN-1998; 98US-0090000.
 PR 19-JUN-1998; 98US-0090003.
 PR 19-JUN-1998; 98US-0090036.
 PR 19-JUN-1998; 98US-0090039.
 PR 19-JUN-1998; 98US-0090040.
 PR 19-JUN-1998; 98US-0090041.
 PR 19-JUN-1998; 98US-0090042.
 PR 19-JUN-1998; 98US-0090043.
 PR 19-JUN-1998; 98US-0090044.
 PR 19-JUN-1998; 98US-0090045.
 PR 19-JUN-1998; 98US-0090047.
 PR 19-JUN-1998; 98US-0090048.
 PR 19-JUN-1998; 98US-0090072.
 PR 19-JUN-1998; 98US-0090076.
 PR 19-JUN-1998; 98US-0090077.
 PR 19-JUN-1998; 98US-0090079.
 PR 19-JUN-1998; 98US-0090079.
 PR 19-JUN-1998; 98US-0090080.
 PR 08-DEC-1998; 98US-0111715.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106077/09.
 XX
 PT Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer -
 XX
 PS Claim 1; Page 115; 130pp; English.
 XX
 CC Sequences AAZ7573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or
 CC ESTs (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can
 CC lyse the tumour cells. Immunostimulatory cofactors also being required
 CC for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen, to modulate the genotype of an APC, to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC, and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell
 CC differentially expressed genes, or of their encoded proteins, can be used
 CC to identify cells as belonging to the monocyte lineage. Cells containing
 CC these genes can be used in active immunotherapy (or to stimulate
 CC production of a population of antigen-specific effector cells) and
 CC vectors containing them are used in gene therapy. Co-administration of
 CC tumour antigens and APC-associated costimulatory factors ensures adequate
 CC antigen presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells.
 XX
 SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

Query Match 34.0%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGGCCAGGC 13
 1 CAGGCTGGC 10

RESULT 288
 AAZ83064/c
 ID AAZ83064 standard; DNA; 10 BP.

AC AAZ83064;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #2298.

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US13647.

PR 19-JUN-1998; 98US-0089853.

PR 19-JUN-1998; 98US-0089997.

PR 19-JUN-1998; 98US-0090039.

PR 19-JUN-1998; 98US-0090040.

PR 19-JUN-1998; 98US-0090041.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

DR WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic

PT and non-metastatic breast cancer cells, useful for diagnosis,

PT prevention and treatment of cancer -

XX Claim 1; Page 121; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct

CC transcripts that are preferentially transcribed in the metastatic breast

CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).

CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts

CC that are preferentially transcribed in the primary or non-metastatic

CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour

CC cells). These transcripts can be used for diagnosis, prognosis,

CC monitoring and treatment of breast cancer, particularly where metastatic.

CC diagnosis is by standard immunoassays or hybridisation/amplification

CC reactions. Compounds that modulate expression of the transcripts are

CC potentially useful for treatment of (metastatic) breast cancer, while

CC promoters from the transcripts are used to direct expression, in selected

CC cell types, of e.g. therapeutic genes (also ribozymes or antisense

CC sequences), particularly an antigen-encoding sequence for use in gene or

CC cell-based vaccines. Polypeptides encoded by the transcripts are also

CC useful in vaccines; for diagnosing breast cancer and for raising

CC specific antibodies (Ab). Ab are used to detect the polypeptides or as

CC therapeutic agents. Host cells that produce the polypeptides can be used

CC to expand and isolate populations of educated, antigen-specific immune

CC effector cells, e.g. cytotoxic T lymphocytes, and these used for

CC adoptive immunotherapy.

XX SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 other;

Query Match 34.0%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CCGGCCCAA 17
 10 CCGGCCCAA 1

RESULT 289
 AAZ83855/c
 ID AAZ83855 standard; DNA; 10 BP.

AC AAZ83855;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #3089.

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US13647.

PR 19-JUN-1998; 98US-0089853.

PR 19-JUN-1998; 98US-0089997.

PR 19-JUN-1998; 98US-0090039.

PR 19-JUN-1998; 98US-0090040.

PR 19-JUN-1998; 98US-0090041.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

DR WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic

PT and non-metastatic breast cancer cells, useful for diagnosis,

PT prevention and treatment of cancer -

XX Claim 1; Page 141; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct

CC transcripts that are preferentially transcribed in the metastatic breast

CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).

CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts

CC that are preferentially transcribed in the primary or non-metastatic

CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour

CC cells). These transcripts can be used for diagnosis, prognosis,

CC monitoring and treatment of breast cancer, particularly where metastatic.

CC diagnosis is by standard immunoassays or hybridisation/amplification

CC reactions. Compounds that modulate expression of the transcripts are

CC potentially useful for treatment of (metastatic) breast cancer, while

CC promoters from the transcripts are used to direct expression, in selected

CC cell types, of e.g. therapeutic genes (also ribozymes or antisense

CC sequences), particularly an antigen-encoding sequence for use in gene or

CC cell-based vaccines. Polypeptides encoded by the transcripts are also

CC useful in vaccines; for diagnosing breast cancer and for raising

CC specific antibodies (Ab). Ab are used to detect the polypeptides or as

CC therapeutic agents. Host cells that produce the polypeptides can be used

CC to expand and isolate populations of educated, antigen-specific immune

CC effector cells, e.g. cytotoxic T lymphocytes, and these used for

CC adoptive immunotherapy.

CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.

XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 other;

Query Match 34.0%; Score 6.8; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 1.8e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

10 GCCGCGCCAA 16

10 GCCGCGCCAA 1

RESULT 290

AA285316

ID AA285316 standard; DNA; 10 BP.

AC AA285316;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell downregulated transcript tag #4550.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

XX antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US13647.

PR 19-JUN-1998; 98US-0089853.

PR 19-JUN-1998; 98US-0089997.

PR 19-JUN-1998; 98US-0090039.

PR 19-JUN-1998; 98US-0090040.

PR 19-JUN-1998; 98US-0090041.

XX (GEN2) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic

PT and non-metastatic breast cancer cells; useful for diagnosis,

PT prevention and treatment of cancer -

XX Claim 1; Page 181; 219pp; English.

XX AA280767 to AA283941 represent tags corresponding to distinct

CC transcripts that are preferentially transcribed in the metastatic breast

CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).

CC AA283942 to AA286677 represent tags corresponding to distinct transcripts

CC that are preferentially transcribed in the primary or non-metastatic

CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour

CC cells). These transcripts can be used for diagnosis, prognosis,

CC monitoring and treatment of breast cancer, particularly where metastatic.

CC Diagnoses is by standard immunoassays or hybridisation/amplification

CC reactions. Compounds that modulate expression of the transcripts are

CC potentially useful for treatment of (metastatic) breast cancer, while

CC promoters from the transcripts are used to direct expression, in selected

CC cell types, of e.g. therapeutic genes (also ribozymes or antisense

CC sequences), particularly an antigen-encoding sequence for use in gene or

CC cell-based vaccines. Polypeptides encoded by the transcripts are also

CC useful in vaccines; for diagnosing breast cancer and for raising

CC specific antibodies (Ab). Ab are used to detect the polypeptides or as

CC therapeutic agents. Host cells that produce the polypeptides can be used
CC to expand and isolate populations of educated, antigen-specific immune
CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
CC adoptive immunotherapy.

XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

Query Match 34.0%; Score 6.8; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 1.8e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4 CCGGCCAGGC 13

1 CAGGCTGGC 10

RESULT 291

AAH64036

ID AAH64036 standard; CDNA; 10 BP.

AC AAH64036;

DT 20-SEP-2001 (first entry)

DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 876.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;

KW cancer diagnosis; cell specific gene expression; ss.

OS Homo sapiens.

PN WO200138577-A2.

PD 31-MAY-2001.

PF 21-NOV-2000; 2000WO-US31922.

PR 24-NOV-1999; 99US-0448480.

PR (UYUO) UNITV JOHNS HOPKINS.

PA Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell

PT type, such as cancer cell, comprises transcriptomes expressed in

PT particular cell types -

XX Claim 13; Page 59; 94pp; English.

XX The present invention describes a method of identifying the type of cell

CC in a sample, involving determining which of the sequences

CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described

CC in the invention are cell-type specific, cancer specific or ubiquitously

CC expressed in humans. They can also be used to screen for drugs, reduce the

CC cancer specific gene expression, standardise expression and restore the

CC function of a diseased cell or tissue. The present sequence is one of

CC the transcriptomes described in the exemplification of the invention.

XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

Query Match 34.0%; Score 6.8; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 1.8e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4 CCGGCCAGGC 13

1 CAGGCTGGC 10

RESULT 292

AAH64037

ID AAH64037 standard; cDNA; 10 BP.
XX
XX AAH64037;
AC
XX
XX
XX 20-SEP-2001 (first entry)
DT
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 877.
DE
XX
XX Human transcriptome; gene expression pattern; cancer; drug screening;
KM cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138577-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 21-NOV-2000; 2000WO-US31922.
PF
XX
XX 24-NOV-1999; 99US-0448480.
PR
XX
XX (UYJO) UNITV JOHNS HOPKINS.
PA
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
DR
XX
XX
XX
XX New isolated polynucleotides, useful for identifying specific cell
PT type, such as cancer cell, comprises transcriptomes expressed in
PT particular cell types -
XX
XX
XX Claim 13; Page 59; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences
CC AAH6161-AAH64724 is expressed by the cell. The transcriptomes described
CC in the invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of
CC the transcriptomes described in the exemplification of the invention.
CC
XX
XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;
SQ
Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CCGGGCCAGC 13
DB 1 CAGGCTTGC 10
RESULT 293
AAK55034
ID AAK55034 standard; DNA; 11 BP.
XX
XX AAK55034;
AC
XX
XX
XX 05-JUL-1999 (first entry)
DT
XX
XX C/EBP-beta antisense oligonucleotide fragment.
DE
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
KM impaired respiration; inflammation; lung disease;
KM pulmonary vasoconstriction; inflammation; allergic rhinitis;
KM acute asthma; allergy; asthma; impeded respiration;
KM respiratory distress syndrome; pain; cystic fibrosis;
KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KM prostate cancer; ss.

XX
XX Synthetic.
OS
XX
XX WO9913886-A1.
PN
XX
XX 25-MAR-1999.
PD
XX
XX 17-SEP-1998; 98WO-US19419.
PF
XX
XX 09-JUN-1998; 98US-0093972.
PR 17-SEP-1997; 97US-0059160.
XX
XX (UYEC-) UNITV EAST CAROLINA.
PA
XX
XX Nyce JW;
PI
XX
XX WPI; 1999-229400/19.
DR
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
PT
XX
XX Disclosure; Page 70; 120pp; English.
PS
XX
XX The specification describes antisense oligonucleotides (AAK52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences AAK55272-74. These multiple target
CC oligonucleotides (specifically AAK55180-271) can be used for the
CC antisense treatment of diseases and conditions. Typical diseases and
CC conditions are those associated with impaired respiration and
CC inflammation, including lung diseases, pulmonary vasoconstriction,
CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC hepatic metastases, as well as all types of cancers which may metastasize
CC or have metastasized to the lungs, including breast and prostate cancer.
CC
XX
XX Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;
SQ
Query Match 34.0%; Score 6.8; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 CCGGGCCAGG 12
DB 2 CCGGGCCCG 11
RESULT 294
AAF20603
ID AAF20603 standard; DNA; 11 BP.
XX
XX AAF20603;
AC
XX
XX
XX 14-MAR-2001 (first entry)
DT
XX
XX Human C/EBP polynucleotide fragment #2170.
DE
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;

KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 cancer; ss.
 XX
 OS Homo sapiens.
 XX WO200062736-A2.
 XX 26-OCT-2000.
 PD
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE-) NYCE J W.
 XX
 PI Nyce JW;
 XX WPI; 2000-679539/66.
 DR
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Claim 14; Page 264; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, anti-inflammatory, analgesic,
 CC immunosuppressive, anticholinergic, hypotensive and cytoskeletal activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy (ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impaired respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;
 Query Match 34.0%; Score 6.8; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 CCGGGCCAGG 12
 DB 2 CCGGGCCCGG 11
 RESULT 295
 AAA34481
 ID AAA34481 standard; DNA; 11 BP.
 XX
 AC AAA34481;
 XX

DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2170.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;
 KW antiallergic; anticholinergic; cytoskeletal; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX 24-FEB-2000.
 PD
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX WPI; 2000-205971/18.
 DR
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Disclosure; Page 537; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 1%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have anti-inflammatory, antiallergic,
 CC anticholinergic, cytoskeletal and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA2333 to AAA3512 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2615, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1880
 CC (AAA2323 to AAA3392) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.
 XX
 SQ Sequence 11 BP; 0 A; 6 C; 5 G; 0 U; 0 other;
 Query Match 34.0%; Score 6.8; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 CCGGGCCAGG 12
 DB 2 CCGGGCCCGG 11

RESULT 296
 ABV68762
 ID ABV68762 standard; cDNA; 11 BP.
 XX
 XX ABV68762;
 AC
 XX 21-OCT-2002 (first entry)
 DT
 XX Human skin EST 6548.
 DE
 XX
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KM immunosuppressive; antinflammatory; cyostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 PD 11-JUL-2002.
 XX
 XX 20-DEC-2001; 2001WO-EP15179.
 PF
 XX 03-JAN-2001; 2001DE-1000127.
 PR
 XX (HENK) HENKEL KGAA.
 PA
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer -
 XX
 PS Disclosure; Page 207; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention.
 CC
 CC
 CC Sequence 11 BP; 1 A; 5 C; 3 G; 2 T; 0 other;
 SQ

Query Match 34.0%; Score 6.8; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 GGCCAGGCCA 15
 |||||
 Db 2 GGCCTGCCCA 11

RESULT 297
 AAX55033
 ID AAX55033 standard; DNA; 12 BP.
 XX
 XX AAX55033;
 AC
 XX 05-JUL-1999 (first entry)
 DT
 XX C/EBP-beta antisense oligonucleotide fragment.
 DE
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 KM impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;

KW acute asthma; allergy; asthma; impeded respiration;
 KM respiratory distress syndrome; pain; cystic fibrosis;
 KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KM prostate cancer; ss.
 XX
 XX Synthetic.
 OS
 XX
 PN WO9913886-A1.
 PD 25-MAR-1999.
 XX
 XX 17-SEP-1998; 98WO-US19419.
 PF
 XX 09-JUN-1998; 98US-0093972.
 PR 17-SEP-1997; 97US-0059160.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX
 PI Nyce JW;
 DR WPI; 1999-229400/19.
 XX
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 PT
 PS Disclosure; Page 70; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juncture between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences AAX55272-74. These multiple target
 CC oligonucleotides (specifically AAX55180-271) can be used for the
 CC antisense treatment of diseases and conditions. Typical diseases and
 CC conditions are those associated with impaired respiration and
 CC inflammation, including lung diseases, pulmonary vasoconstriction,
 CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
 CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
 CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
 CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
 CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
 CC hepatic metastases, as well as all types of cancers which may metastasize
 CC or have metastasized to the lungs, including breast and prostate cancer.
 CC
 CC
 CC Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;
 SQ

Query Match 34.0%; Score 6.8; DB 1; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 CCGGCGCAGG 12
 |||||
 Db 3 CCGGCGCCGG 12

RESULT 298
 AAF20602
 ID AAF20602 standard; DNA; 12 BP.
 XX
 XX AAF20602;
 AC
 XX 14-MAR-2001 (first entry)
 DT
 XX Human C/EBP polynucleotide fragment #2169.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 XX
 XX Homo sapiens.
 OS
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000MO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 PI
 PI Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 XX Claim 14; Page 264; 1592pp; English.
 BS
 XX
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors, and
 CC immunoglobulin and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 CC
 XX Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;
 SQ
 QY Query Match 34.0%; Score 6.8; DB 1; Length 12;
 Db Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 299
 AAA34480
 ID AAA34480 standard; DNA; 12 BP.
 XX
 XX AAA34480;
 AC
 XX
 XX 28-JUL-2000 (first entry)
 DT
 XX
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2169.
 DE
 XX
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KM phosphorothioate; impeded respiration; inflammation; allergy;
 KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KM antiasthmatic; cytostatic; analgesic; impeded airway;
 KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 XX
 XX Homo sapiens.
 OS
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99MO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA
 PI
 PI Nyce JW;
 XX
 XX WPI; 2000-205971/18.
 DR
 XX
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 XX Disclosure; Page 537; 1343pp; English.
 PS
 XX
 XX The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA3233 to AAA3312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA3233 to AAA3392) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.
 CC
 XX Sequence 12 BP; 0 A; 7 C; 5 G; 0 U; 0 other;
 SQ
 QY Query Match 34.0%; Score 6.8; DB 1; Length 12;
 Db Best Local Similarity 80.0%; Pred. No. 2.4e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 CCGGGCCAGG 12
 |||||
 Db 3 CCGGGCCCGG 12

RESULT 300

AAX29560

ID AAX29560 standard; DNA; 8 BP.

AC AAX29560;

DT 03-JUN-1999 (first entry)

DE Primer for human G-protein coupled receptor genes.

KW Nucleic acid amplification; nuclear receptor; G-protein coupled receptor;
 KW apoptosis; DNA repair; DNA replication; plant biology; agriculture;
 KW human; veterinary medicine; reproduction; microbiology; hybridisation;
 KW environmental science; DNA fingerprinting; PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

PN MO9911823-A2.

PD 11-MAR-1999.

PF 04-SEP-1998; 98WO-US18392.

PR 05-SEP-1997; 97US-0925816.

PA (KIMM-) KIMMEL CANCER CENT SIDNEY.

PI McClelland M, Pesole G;

DR WPI; 1999-205200/17.

PT Subset of primers able to amplify group of related sequences

PS Claim 21; Page 75; 92pp; English.

CC The invention provides primers (AAX29501-X29679) for identifying
 CC sequences encoding structurally or functionally related proteins such as
 CC nuclear or G-protein coupled receptors; apoptosis-related or DNA
 CC repair/replication proteins. The identified sequences are broadly useful
 CC in plant biology, agriculture, human or veterinary medicine,
 CC reproduction, microbiology or environmental science, e.g. to study
 CC expression of nuclear receptors at different stages of tissue development
 CC or after treatment with particular drugs. It is also used for DNA
 CC fingerprinting (to generate products useful for differential
 CC hybridisation), or, where a 3'-anchor primer is used, to isolate the
 CC 3'-ends of mRNA sequences. Sequences AAX29526-X29583 represent claimed
 CC primers specific for human G-protein coupled receptor genes.

SQ Sequence 8 BP; 0 A; 4 C; 2 G; 2 T; 0 other;

Query Match 32.0%; Score 6.4; DB 1; Length 8;

Best Local Similarity 87.5%; Pred. No. 5.8e+02; Mismatches 1; Indels 0; Gaps 0;

OY 2 TCCGGGCC 9
 |||||

Db 1 TCCTGGCC 8

Search completed: November 10, 2003, 08:01:33
 Job time : 2 secs


```

; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; MEDIUM TYPE: STORAGE
; COMPUTER: PENTIUM
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,629A
; FILING DATE: August 13, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-910-629A-31

```

```

Query Match          100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1  GTCCGGGCGCCAGGCCAAGTC 20
          |||
Db      1  GTCCGGGCGCCAGGCCAAGTC 20

```

```

RESULT 2
US-08-910-629A-42/c
; Sequence 42, Application US/08910629A
; Patent No. 5877309
; GENERAL INFORMATION:
; APPLICANT: Robert A. McKay
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; MEDIUM TYPE: STORAGE
; COMPUTER: PENTIUM
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,629A
; FILING DATE: August 13, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
; US-08-910-629A-42

```

```

Query Match          100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1  GTCCGGGCGCCAGGCCAAGTC 20
          |||
Db      20 GTCCGGGCGCCAGGCCAAGTC 1

```

```

RESULT 3
US-09-209-668-7
; Sequence 7, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: ALPHA-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
; US-09-209-668-7

```

```

Query Match          100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1  GTCCGGGCGCCAGGCCAAGTC 20
          |||
Db      1  GTCCGGGCGCCAGGCCAAGTC 20

```

```

RESULT 4
US-09-287-796-31
; Sequence 31, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPH-0350
; CURRENT APPLICATION NUMBER: US/09/287,796A
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/130,616
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629

```

EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 31
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-287-796-31

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGGCGAGCCCAAGTC 20
DB 1 GTCCGGGCGAGCCCAAGTC 20

RESULT 5
US-09-287-796-42/C

Sequence 42, Application US/09287796A
Patent No. 6133246
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0350
CURRENT APPLICATION NUMBER: US/09/287,796A
EARLIER FILING DATE: 1999-04-07
EARLIER APPLICATION NUMBER: 09/130,616
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 42
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-287-796-42

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGGCGAGCCCAAGTC 20
DB 20 GTCCGGGCGAGCCCAAGTC 1

RESULT 6
US-09-130-616-31

Sequence 31, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03

NUMBER OF SEQ ID NOS: 178
SEQ ID NO 31
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-130-616-31

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGGCGAGCCCAAGTC 20
DB 1 GTCCGGGCGAGCCCAAGTC 20

RESULT 7
US-09-130-616-42/C

Sequence 42, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 42
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-130-616-42

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGGCGAGCCCAAGTC 20
DB 20 GTCCGGGCGAGCCCAAGTC 1

RESULT 8
US-09-371-772B-6740/C

Sequence 6740, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
LEVELS OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (1237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
EARLIER FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225

SOFTWARE: Patentin version 3.0
SEQ ID NO 6740
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-6740

Query Match 77.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 CCGGGCCAGGCCAAGTC 19
Db 17 CCGGGCCAGGCCAAGTC 1

RESULT 9
US-08-951-923-51

Sequence 51, Application US/08951923
Patent No. 6048693

GENERAL INFORMATION:

APPLICANT: Bitter, Grant

TITLE OF INVENTION: PHENOTYPIC ASSAYS OF CYCLIN/CYCLIN-DEPENDENT KINASE

TITLE OF INVENTION: FUNCTION

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward LLP

STREET: 5 Palo Alto Square, 3000 El Camino Real

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94306-2155

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/951,923

FILING DATE: October 16, 1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Neeley, Richard L.

REGISTRATION NUMBER: 30,092

REFERENCE/DOCKET NUMBER: BITT-001/02US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650 843-5000

TELEFAX: 650 857-0663

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 18

TYPE: nucleic acid

STRANDEDNESS: single stranded

TOPOLOGY: linear

MOLECULE TYPE: DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-951-923-51

Query Match 77.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.4;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CCGGGCCAGGCCAAGTC 20
Db 2 CCGGGCCAGGCCAAGTC 18

RESULT 10
US-08-584-040-6244/C

Sequence 6244, Application US/08584040

Patent No. 6346398

GENERAL INFORMATION:

APPLICANT: Pavco, Pamela

APPLICANT: McSwigen, James

APPLICANT: Stinchcomb, Dan T.

TITLE OF INVENTION: Escobedo, Jaime

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: TREATMENT OF DISEASES OR

TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

TITLE OF INVENTION: GROWTH FACTOR

NUMBER OF SEQUENCES: 8502

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/005,974

FILING DATE: October 26, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/064

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 6244:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-584-040-6244

Query Match 74.0%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.5;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 CCGGGCCAGGCCAAGTC 20
Db 18 CCGGGCCAGGCCAAGTC 1

RESULT 11
US-09-371-772B-3004/C
Sequence 3004, Application US/09371772B

Patent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwigen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

FILE REFERENCE: MBH800,876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772B

CURRENT FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3004
LENGTH: 18
TYPE: RNA
ORGANISM: Mus sp.
US-09-371-772B-3004

Query Match 74.0%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.5;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGCCAAGTC 20
DB 18 CCGGGCCAGGCCAAGTC 1

RESULT 12
US-08-584-040-4222/c
Sequence 4222, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4222:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-4222
Query Match 72.0%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 5.9;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGCCAAG 18
DB 16 CCGGGCCAGGCCAAG 1

RESULT 13
US-09-371-772B-1989/c
Sequence 1989, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MHB00,876-J(237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1989
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-1989

Query Match 72.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5.9;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGCCAAG 18
DB 16 CCGGGCCAGGCCAAG 1

RESULT 14
US-08-584-040-7661/c
Sequence 7661, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7661:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-584-040-7661
```

```

Query Match          70.0%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 GCCAGGCCCAAGTC 20
Db 17 GCCAGGCCCAAGTC 4
```

```

RESULT 15
US-09-371-772B-3450/C
; Sequence 3450, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH800, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3450
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
;
US-09-371-772B-3450
```

```

Query Match          70.0%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 GCCAGGCCCAAGTC 20
Db 17 GCCAGGCCCAAGTC 4
```

```

RESULT 16
US-09-371-772B-4833/C
; Sequence 4833, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Elledge, Stephen J.
```

```

; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH800, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4833
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-09-371-772B-4833
```

```

Query Match          69.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.5;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 CCGGGCCAGGCCCAACT 19
Db 17 CCGGGCCAGGCCCAACT 1
```

```

RESULT 17
US-09-371-772B-5851/C
; Sequence 5851, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH800, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5851
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-09-371-772B-5851
```

```

Query Match          67.0%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 8;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 CCGGGCCAGGCCCAA 17
Db 16 CCGGGCCAGGCCCAA 2
```

```

RESULT 18
US-08-924-183-6
; Sequence 6, Application US/08924183A
; Patent No. 6218109
; GENERAL INFORMATION:
; APPLICANT: Elledge, Stephen J.
```



```

; APPLICANT: Sanchez, Yolanda
; TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
; FILE REFERENCE: 120541-1003
; CURRENT APPLICATION NUMBER: US/08/924,183A
; CURRENT FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-924-183-6

Query Match      67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 8.8;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GGGCAGGCCAAAGTC 20
Db      3 GGACAGGCCAAAGTC 17

RESULT 19
US-09-488-364-6
; Sequence 6, Application US/09488364
; Patent No. 6307015
; GENERAL INFORMATION:
; APPLICANT: Elledge, Stephen J.
; APPLICANT: Sanchez, Yolanda
; TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
; FILE REFERENCE: 120541-1013
; CURRENT APPLICATION NUMBER: US/09/488,364
; CURRENT FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-488-364-6

Query Match      67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 8.8;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GGGCAGGCCAAAGTC 20
Db      3 GGACAGGCCAAAGTC 17

RESULT 20
US-08-584-040-1996/C
; Sequence 1996, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
```

```

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1996:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-1996

Query Match      67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 8.8;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCGGGCCAGGCCAAA 17
Db      15 CCGGGCCAGGCCAAA 1

RESULT 21
US-09-371-772B-541/C
; Sequence 541, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re)
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEH800.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 541
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-541

Query Match      67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 8.8;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 3 CCGGGCCAGGCCCAA 17
Db 15 CCGGGCCAGGCCCAA 1

RESULT 22

US-09-371-772B-4834/c
Sequence 4834, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MHB00,876-0 (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4834
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-4834

Query Match
Best Local Similarity 67.0%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGCCCAA 17
Db 16 CCGGGCCAGGCCCAA 2

RESULT 23

US-08-584-040-7660/c
Sequence 7660, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7660:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-7660

Query Match
Best Local Similarity 65.0%; Score 13; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCAAAGTC 20
Db 17 CCAGGCCAAAGTC 5

RESULT 24

US-09-371-772B-3449/c
Sequence 3449, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MHB00,876-0 (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3449
LENGTH: 17
TYPE: RNA
ORGANISM: Mus sp.
US-09-371-772B-3449

Query Match
Best Local Similarity 65.0%; Score 13; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCAAAGTC 20
Db 17 CCAGGCCAAAGTC 5

RESULT 25

US-08-584-040-5795/c
Sequence 5795, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.

APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5795:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-5795

Query Match 64.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGCCAAG 18
DB 16 CCGGGCCAGGCCAAG 1

RESULT 26
US-09-371-772B-2661/C
Sequence 2661, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH800,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PatentIn version 3.0
SEQ ID NO 2661
LENGTH: 17
TYPE: RNA
ORGANISM: Mus sp.
US-09-371-772B-2661

Query Match 64.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGCCAAG 18
DB 16 CCGGGCCAGGCCAAG 1

RESULT 27
US-08-822-586-49/C
Sequence 49, Application US/08822586
Patent No. 6015890
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
APPLICANT: AMALIO TELENTE
TITLE OF INVENTION: AN EMBICAB OPERON OF MYCOBACTERIA AND
MUTANTS THEREOF
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/437
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 OR 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
US-08-822-586-49

Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGCCAA 16
DB 12 GGGCCAGGCCCA 1

RESULT 28
US-09-281-418-100
Sequence 100, Application US/09281418
Patent No. 6287769

GENERAL INFORMATION:
APPLICANT: Inoue, Takakazu
TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi
TITLE OF INVENTION: nisms and Method of Assaying Contaminant
FILE REFERENCE: 9982-7
CURRENT APPLICATION NUMBER: US/09/281,418
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: JP/1998/87651
EARLIER FILING DATE: 1998-03-31
EARLIER APPLICATION NUMBER: JP/1999/69694
EARLIER FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 216
SEQ ID NO 100
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-281-418-100

Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CAGGCCCAAGTC 20
1 CAGGCCCAAGTC 12

RESULT 29
US-08-882-046-77/c
Sequence 77, Application US/08882046
Patent No. 6136952

GENERAL INFORMATION:
APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Krantz, Ian D.
APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-882-046-77

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGGCCAGGCCAA 17
13 GGGCCAGGCCACA 1

RESULT 30
US-09-922-445-11
Sequence 11, Application US/09922445
Patent No. 6528268
GENERAL INFORMATION:
APPLICANT: Andersson, Maria K.
APPLICANT: Berglund, Lars G. T.
APPLICANT: Reneland, Rikard H.
APPLICANT: Adam, Gail I. R.
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
FILE REFERENCE: G3126US
CURRENT APPLICATION NUMBER: US/09/922,445
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 13
TYPE: DNA
ORGANISM: synthetic
US-09-922-445-11

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGGCCAGGCCA 15
1 CCGGCCAGGCCA 13

RESULT 31
US-09-922-445-36/c
Sequence 36, Application US/09922445
Patent No. 6528268
GENERAL INFORMATION:
APPLICANT: Andersson, Maria K.
APPLICANT: Berglund, Lars G. T.
APPLICANT: Reneland, Rikard H.
APPLICANT: Adam, Gail I. R.
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
FILE REFERENCE: G3126US
CURRENT APPLICATION NUMBER: US/09/922,445
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.1
SEQ ID NO 36
LENGTH: 13
TYPE: DNA
ORGANISM: synthetic
US-09-922-445-36

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGGCCAGGCCA 15
13 CCGGCCAGGCCA 1

RESULT 32
US-09-249-155A-324
Sequence 324, Application US/09249155A
Patent No. 6538173

GENERAL INFORMATION:
APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
FILE REFERENCE: 00486.78503
CURRENT APPLICATION NUMBER: US/09/249,155A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,737
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/097,937
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: US 60/102,051
PRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 346
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 324
LENGTH: 11
TYPE: DNA
ORGANISM: Mus musculus
US-09-249-155A-324

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCCGGGCCAGG 12
Db 1 TCCGGGCCAGG 11

RESULT 33
US-08-951-923-51/C
Sequence 51, Application US/08951923
Patent No. 6048693
GENERAL INFORMATION:
APPLICANT: Bitter, Grant
TITLE OF INVENTION: PHENOTYPIC ASSAYS OF CYCLIN/CYCLIN-DEPENDENT KINASE
TITLE OF INVENTION: FUNCTION
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward LLP
STREET: 5 Palo Alto Square, 3000 El Camino Real
City: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,923
FILING DATE: October 16, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neelley, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: BITT-001/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650 843-5000
TELEFAX: 650 857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-951-923-51

Query Match 44.0%; Score 8.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCCAGGCCAAA 17
Db 12 GGCCCTGGCCAGA 1

RESULT 34
US-08-388-353-387
Sequence 387, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Leamont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
City: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4356
TELEX: 230 901.SANS UR
INFORMATION FOR SEQ ID NO: 387:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-387

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGG 12
Db 1 CAGGGCCAGG 10

RESULT 35
US-08-488-551B-387
Sequence 387, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 96062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 387:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
type: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-387

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGGCCAGG 12
DB 1 CAGGGCCAGG 10

RESULT 36
US-08-522-384-63/c
Sequence 63, Application US/08522384
Patent No. 6110667
GENERAL INFORMATION:
APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: NIGAM, SANJAY KIMAR
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
FILE REFERENCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 63
LENGTH: 10
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-63

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCGGGCCAGG 13
DB 10 CAGGGCCAGG 1

RESULT 37
US-09-720-201A-24
Sequence 24, Application US/09720201A
Patent No. 6524853
GENERAL INFORMATION:
APPLICANT: KOHARA, MICHINORI
APPLICANT: KOHARA, KYOKO
APPLICANT: TAIRA, KAZUWARI
APPLICANT: MATSUZAKI, JUNICHI
APPLICANT: OHMORI, HIROSHI
TITLE OF INVENTION: A VECTOR EXPRESSING AN RNA VIRAL FULL-LENGTH GENE AND
TITLE OF INVENTION: ITS USE
FILE REFERENCE: 04853.0051-00000
CURRENT APPLICATION NUMBER: US/09/720,201A
CURRENT FILING DATE: 2000-12-22
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 98/177,820
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: PCT/JP99/03381
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 24
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-720-201A-24

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGCC 14
DB 1 GGGCCAGGCC 10

RESULT 38
US-08-822-586-49
Sequence 49, Application US/08822586
Patent No. 6015890
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
APPLICANT: AMALIO TELENTE
TITLE OF INVENTION: AN EMBCA OPERON OF MYCOBACTERIA AND
TITLE OF INVENTION: MUTANTS THEREOF
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,586
FILING DATE: MARCH 20, 1997

ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/437
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 286-0854 or 286-0082
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
US-08-822-586-49

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCAGGCC 14
DB 2 GGGCCTGGCC 11

RESULT 39
US-08-859-954-105
Sequence 105, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramtin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES

ANTI-SENSE: YES
US-08-859-954-105

Query Match 40.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCAAGT 19
DB 1 GCCAAGT 8

RESULT 40
US-08-441-887A-183/C
Sequence 183, Application US/08441887A
Patent No. 5837832
GENERAL INFORMATION:
APPLICANT: Chee, Mark
APPLICANT: Cronin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Hubbard, Earl A.
APPLICANT: Lipschutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-326-2400
TELEFAX: 650-326-2422
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (probe)
US-08-441-887A-183

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCCGGGCC 9

Db 8 TCCGGGCC 1

RESULT 41

US-08-192-942-6/c
Sequence 6, Application US/08192942
Patent No. 5989906
GENERAL INFORMATION:
APPLICANT: JAMES D. THOMPSON
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING P-GLYCOPROTEIN mdr-
TITLE OF INVENTION: 1 GENE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/192,942
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/882,885
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/173
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-192-942-6

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCAAGT 19
Db 10 GCCAAGT 3

RESULT 42

US-08-388-353-388
Sequence 388, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza

CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DiGiullo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 388:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-388

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGCCGAG 12
Db 2 GGCCGAG 9

RESULT 43

US-08-388-353-389
Sequence 389, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DiGiullo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366
TELEX: 230 301 SANS UR
INFORMATION FOR SEQ ID NO: 389:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-389

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCCAG 12
DB 1 GGGCCAG 8

RESULT 44
US-08-488-551B-388
Sequence 388, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGILIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 388:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-388

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 32;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCCAG 12
DB 2 GGGCCAG 9

RESULT 45
US-08-488-551B-389
Sequence 389, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGILIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 389:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-389

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCCAG 12
DB 1 GGGCCAG 8

RESULT 46
US-08-924-183-6/C
Sequence 6, Application US/08924183A
Patent No. 6218109
GENERAL INFORMATION:
APPLICANT: Ellledge, Stephen J.

APPLICANT: Sanchez, Yolanda
TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
FILE REFERENCE: 120541-1003
CURRENT APPLICATION NUMBER: US/08/924,183A
CURRENT FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-924-183-6

Query Match
Best Local Similarity 39.0%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCCAGGCCAA 16
Db 11 GGCCTGTCCAA 1

RESULT 47
US-09-488-364-6/C
Sequence 6, Application US/09488364
Patent No. 6307015
GENERAL INFORMATION:
APPLICANT: Elledge, Stephen J.
APPLICANT: Sanchez, Yolanda
TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
FILE REFERENCE: 120541-1013
CURRENT APPLICATION NUMBER: US/09/488,364
CURRENT FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-488-364-6

Query Match
Best Local Similarity 39.0%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCCAGGCCAA 16
Db 11 GGCCTGTCCAA 1

RESULT 48
US-08-910-629A-31/C
Sequence 31, Application US/08910629A
Patent No. 5877309
GENERAL INFORMATION:
APPLICANT: Robert A. McKay
APPLICANT: Nicholas M. Dean
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: PENTIUM
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,629A
FILING DATE: August 13, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-910-629A-31

Query Match
Best Local Similarity 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCC 14
Db 14 GGCCTGCCCCGAC 1

RESULT 49
US-08-910-629A-42
Sequence 42, Application US/08910629A
Patent No. 5877309
GENERAL INFORMATION:
APPLICANT: Robert A. McKay
APPLICANT: Nicholas M. Dean
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: PENTIUM
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,629A
FILING DATE: August 13, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257

```

; REFERENCE/DOCKET NUMBER: ISPH-0215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
; US-08-910-629A-42

Query Match          38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GTCCGGGCGCAGGCC 14
Db      7  GGCCTGGCCCGGAC 20

RESULT 50
US-09-209-668-7/c
; Sequence 7, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monla, Brett P.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0316
; CURRENT APPLICATION NUMBER: US/09/209,668A
; EARLIER FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
; US-09-209-668-7

Query Match          38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GTCCGGGCGCAGGCC 14
Db      14 GGCCTGGCCCGGAC 1

RESULT 51
US-09-287-796-31/c
; Sequence 31, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monla, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0350
; CURRENT APPLICATION NUMBER: US/09/287,796A
; EARLIER FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/130,616
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
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```

; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-09-287-796-31

Query Match          38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GTCCGGGCGCAGGCC 14
Db      14 GGCCTGGCCCGGAC 1

RESULT 52
US-09-287-796-42
; Sequence 42, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monla, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0350
; CURRENT APPLICATION NUMBER: US/09/287,796A
; EARLIER FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/130,616
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-09-287-796-42

Query Match          38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GTCCGGGCGCAGGCC 14
Db      7  GGCCTGGCCCGGAC 20

RESULT 53
US-09-130-616-31/c
; Sequence 31, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monla, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 31
```

LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-130-616-31

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCCGGCCGAGCC 14
Db 14 GGCGTGGCCGAGC 1

RESULT 54
US-09-130-616-42
Sequence 42, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Bretc
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 42
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-130-616-42

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCCGGCCGAGCC 14
Db 7 GGCGTGGCCGAGC 20

RESULT 55
US-08-105-483-423
Sequence 423, Application US/08105483
Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: Pacietti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 423:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-423

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1,6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGCCCAA 17
Db 1 GGCCCAA 7

RESULT 56
US-08-709-209-423
Sequence 423, Application US/08709209
Patent No. 5762938
GENERAL INFORMATION:
APPLICANT: Pacietti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILING DATE: 21-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 423:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-709-209-423

Query Match          35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GGCCTAA 17
Db      1 GGCCTAA 7

RESULT 57
US-08-303-275-131
; Sequence 131, Application US/08303275
; Patent No. 5766598
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS RECOMBINANT
; TITLE OF INVENTION: FOXPVIRUS VACCINE
; NUMBER OF SEQUENCES: 205
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,275
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,382
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2420
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-303-275-131

Query Match          35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GGCCTAA 17
Db      1 GGCCTAA 7

RESULT 58
US-08-458-101-423
; Sequence 423, Application US/08458101
; Patent No. 5766599
; GENERAL INFORMATION:
```

```
; APPLICANT: Paoletti, Enzo
; APPLICANT: Perkus, Marion E.
; APPLICANT: Taylor, Jill
; APPLICANT: Tartaglia, James
; APPLICANT: No. 5766599con, Elizabeth K.
; APPLICANT: Riviere, Michel
; APPLICANT: de Taisne, Charles
; APPLICANT: Limbach, Keith J.
; APPLICANT: Johnson, Gerard P.
; APPLICANT: Pincus, Steven E.
; APPLICANT: Cox, William I.
; APPLICANT: Audonnet, Jean-Christophe Francis
; APPLICANT: Gettig, Russell Robert
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; TITLE OF INVENTION: STRAIN
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,101
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2740
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 423:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-458-101-423

Query Match          35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GGCCTAA 17
Db      1 GGCCTAA 7

RESULT 59
US-08-859-954-106
; Sequence 106, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
```

COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-106

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCAAG 18
Db 1 GCCAAG 7

RESULT 60
US-08-859-954-359
Sequence 359, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-359

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCAAGT 19
Db 2 CCAAGT 8

RESULT 61
US-08-474-700B-43/C
Sequence 43, Application US/08474700B
Patent No. 6001990
GENERAL INFORMATION:
APPLICANT: Wands, Jack
APPLICANT: Wakita, Takaji
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
TITLE OF INVENTION: VIRUS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,700B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,382
FILING DATE: 10 May 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/279001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-474-700B-43

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GCCAGGCC 14
Db 8 GCCAGGCC 1

RESULT 62
US-08-859-954-56
Sequence 56, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramon
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-56

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GCCAAACT 19
Db 1 GCCAAACT 8

RESULT 63
US-08-859-954-107
Sequence 107, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.

APPLICANT: Homayouni, Ramon
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-107

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GCCAAACT 19
Db 1 GCCAAACT 8

RESULT 64
US-09-041-675-9/c
Sequence 9, Application US/09041675A
Patent No. 6100032
GENERAL INFORMATION:
APPLICANT: Kern, Scott
APPLICANT: Zavel, Leigh
APPLICANT: Dai, Jia Le
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Human SMAD3 and SMAD4 are
FILE REFERENCE: 01107.74098
CURRENT APPLICATION NUMBER: US/09/041,675A
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 8
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: synthetic random oligonucleotides selected for
OTHER INFORMATION: binding to human SMAD3 or human SMAD4
US-09-041-675-9

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 GCGCAGGC 13
DB 8 GCGCAGGC 1

RESULT 65
US-09-041-675-15
Sequence 15, Application US/09041675A
Patent No. 6100032
GENERAL INFORMATION:
APPLICANT: Kern, Scott
APPLICANT: Zewel, Leigh
APPLICANT: Dai, Jia Le
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Human SMAD3 and SMAD4 are
FILE REFERENCE: 01107.74098
CURRENT APPLICATION NUMBER: US/09/041.675A
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 8
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic random oligonucleotides selected for
OTHER INFORMATION: binding to human SMAD3 or human SMAD4
US-09-041-675-15

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGCGGC 8
DB 1 GTCGCGGC 8

RESULT 66
US-09-041-675-23
Sequence 23, Application US/09041675A
Patent No. 6100032
GENERAL INFORMATION:
APPLICANT: Kern, Scott
APPLICANT: Zewel, Leigh
APPLICANT: Dai, Jia Le
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Human SMAD3 and SMAD4 are
FILE REFERENCE: 01107.74098
CURRENT APPLICATION NUMBER: US/09/041.675A
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 8
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic random oligonucleotides selected for
OTHER INFORMATION: binding to human SMAD3 or human SMAD4

US-09-041-675-23

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGCGGC 8
DB 1 GTCGCGGC 8

RESULT 67
US-08-646-301A-10
Sequence 10, Application US/08646301A
Patent No. 6194211
GENERAL INFORMATION:
APPLICANT: Richards, Cynthia Ann
APPLICANT: Huber, Brian E.
TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
FILE REFERENCE: PB1508USW
CURRENT APPLICATION NUMBER: US/08/646.301A
CURRENT FILING DATE: 1996-05-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 8
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
OTHER INFORMATION: sequence B4 from DNA Sequence 1:3-11 (1990).
Patent No. 6194211
US-08-646-301A-10

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCGCAGGC 14
DB 1 GSSWGCSC 8

RESULT 68
US-08-646-301A-10/c
Sequence 10, Application US/08646301A
Patent No. 6194211
GENERAL INFORMATION:
APPLICANT: Richards, Cynthia Ann
APPLICANT: Huber, Brian E.
TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
FILE REFERENCE: PB1508USW
CURRENT APPLICATION NUMBER: US/08/646.301A
CURRENT FILING DATE: 1996-05-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 8
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
OTHER INFORMATION: sequence B4 from DNA Sequence 1:3-11 (1990).
Patent No. 6194211
US-08-646-301A-10

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGCAGGC 13
DB 8 GCGCAGGC 1
RESULT 69
US-09-398-499-16/C
; Sequence 16, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-16
Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GCGCAGGC 11
DB 8 GCGCAGGC 1
RESULT 70
US-09-398-499-39
; Sequence 39, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 39
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-39
Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GCGCAGGC 11
DB 1 GCGCAGGC 8
RESULT 71
US-08-522-384-63
; Sequence 63, Application US/08522384
; Patent No. 610667
; GENERAL INFORMATION:

APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: NIGAM, SANJAY KUMAR
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
FILE REFERENCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 63
LENGTH: 10
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-63
Query Match 32.0%; Score 6.4; DB 1; Length 10;
Best Local Similarity 87.5%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCGCAGGC 14
DB 1 GCGCAGGC 8
RESULT 72
US-08-584-040-7661
; Sequence 7661, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7661:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-7661

Query Match 32.0%; Score 6.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGGCAGGC 13
DB 10 GGGCUGGC 17

RESULT 73
US-09-371-772B-3450
Sequence 3450, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggan, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3450
LENGTH: 17
TYPE: RNA
ORGANISM: Mus sp.
US-09-371-772B-3450

Query Match 32.0%; Score 6.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGGCAGGC 13
DB 10 GGGCUGGC 17

RESULT 74
US-07-949-541A-34/C
Sequence 34, Application US/07949541A
Patent No. 5552270
GENERAL INFORMATION:
APPLICANT: Khripko, Konstantin R.
APPLICANT: Khorlin, Alexandr A.
APPLICANT: Ivanov, Igor B.
APPLICANT: Ershov, Gennady M.
APPLICANT: Lysov, Yuri P.
APPLICANT: Florentiev, Vladimir L.
APPLICANT: Mirzabekov, Andrei D.
TITLE OF INVENTION: Method for Determining a DNA Nucleotide
TITLE OF INVENTION: Sequence and a Device for Carrying Out Same
Patent No. 5552270
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladase & Parry
STREET: 26 West 61st Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC/XT/AT or compatibles
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/949,541A
FILING DATE: 09-No. 5552270-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/RU92/00052
FILING DATE: 18-Mar-1992
APPLICATION NUMBER: Russian Federation 4919321
FILING DATE: 18-Mar-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet I. Cord
REGISTRATION NUMBER: 33,778
REFERENCE/DOCKET NUMBER: U-8999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
TELEX: 233288
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: chemically synthesized
FEATURE: oligonucleotide was synthesized by phosphoramidite
FEATURE: method
OTHER INFORMATION: Letter M means the tethering to the
OTHER INFORMATION: support via oxidized 3-methyluridine.
US-07-949-541A-34

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1,6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCAG 11
DB 6 GGGCAG 1

RESULT 75
US-07-949-541A-39/C
Sequence 39, Application US/07949541A
Patent No. 5552270
GENERAL INFORMATION:
APPLICANT: Khripko, Konstantin R.
APPLICANT: Khorlin, Alexandr A.
APPLICANT: Ivanov, Igor B.
APPLICANT: Ershov, Gennady M.
APPLICANT: Lysov, Yuri P.
APPLICANT: Florentiev, Vladimir L.
APPLICANT: Mirzabekov, Andrei D.
TITLE OF INVENTION: Method for Determining a DNA Nucleotide
TITLE OF INVENTION: Sequence and a Device for Carrying Out Same
Patent No. 5552270
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladase & Parry
STREET: 26 West 61st Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC/XT/AT or compatibles
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/949,541A
FILING DATE: 09-Mar-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/RU92/00052
FILING DATE: 18-Mar-1992
APPLICATION NUMBER: Russian Federation 4919321
FILING DATE: 18-Mar-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet I. Cord
REGISTRATION NUMBER: 33,778
REFERENCE/DOCKET NUMBER: U-8999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
TELEX: 233288
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: chemically synthesized
MOLECULE TYPE: deoxyribonucleotide.
FEATURE: oligonucleotide was synthesized by phosphoramidite
FEATURE: method.
OTHER INFORMATION: letter M means the tethering to the
OTHER INFORMATION: support via oxidized 3-methyluridine.
US-07-949-541A-39

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCACG 11
7 GGCACG 2

Db 7 GGCACG 2

RESULT 76
US-08-593-345B-13/C
Sequence 13, Application US/08593345B
Patent No. 5851772
GENERAL INFORMATION:
APPLICANT: Mirzabekov, Andrei D
APPLICANT: Lysov, Yuriy P
APPLICANT: Shick, Valentine V
APPLICANT: Dubiley, Svetlana A
TITLE OF INVENTION: A Microchip Method for the Enrichment of
TITLE OF INVENTION: Specific DNA Sequences.
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHERSKOV & FLAYNIK
STREET: 20 N. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.4 MB storage
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/593,345B
FILING DATE: 29-JAN-96
PRIOR APPLICATION DATA: No. 5851772e
ATTORNEY/AGENT INFORMATION:
NAME: Cherskov, Michael J
REGISTRATION NUMBER: 33,664
REFERENCE/DOCKET NUMBER: ANL-IN-95-029+30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 621-1330
TELEFAX: (312) 621-0088

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 bases
TYPE: nucleic acid
STRANDEDNESS: No. 5851772 Applicable
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: No. 5851772e
LOCATION: 1-8
IDENTIFICATION METHOD: Similarity with known sequences.
OTHER INFORMATION: Complementarity with primer of
OTHER INFORMATION: exons to a-thalassemia gene.
US-08-593-345B-13

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGCCAA 16
8 GGCCAA 3

Db 8 GGCCAA 3

RESULT 77
US-08-859-954-53/C
Sequence 53, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-53

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 15 AAGTC 20
|||||
Db 8 AAGTC 3

RESULT 78
US-08-859-954-81/c
; Sequence 81, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-81

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 13 CCAAG 18
|||||
Db 7 CCAAG 2

RESULT 79
US-08-859-954-104
; Sequence 104, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.

APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-104

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 12 GCCAA 17
|||||
Db 1 GCCAA 6

RESULT 80
US-08-859-954-329/c
; Sequence 329, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-104

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 329:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-329

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AAGTC 20
|||||
Db 8 AAGTC 3

RESULT 81
US-08-859-954-332
Sequence 332, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325

TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 332:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-332

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CAAAGT 19
|||||
Db 3 CAAAGT 8

RESULT 82
US-08-859-954-333/C
Sequence 333, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 333:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-333

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      13 CCAAG 18
        |||||
Db       7 CCAAG 2

RESULT 83
US-08-859-954-360
; Sequence 360, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramtin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-360

Query Match      30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      13 CCAAG 18
        |||||
Db       2 CCAAG 7

RESULT 84
US-08-859-954-396
; Sequence 396, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramtin
; APPLICANT: Hardin, Paul E.

```

```

; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-396

Query Match      30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      11 GGCAA 16
        |||||
Db       3 GGCAA 8

```

Search completed: November 10, 2003, 08:03:59
 Job time : 1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model1

Run on: November 10, 2003, 08:06:57 ; Search time 0.001 Seconds
(without alignments)
27.440 Million cell updates/sec

Title: us-09-774-809-31

Perfect score: 20
Sequence: 1 gtcgsgcgccagcgcaagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 63 seqs, 686 residues

Total number of hits satisfying chosen parameters: 126

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 86 summaries

Database: rnpb.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	20 1 US-09-774-809-31	Sequence 31, Appl
2	20	100.0	20 1 US-09-774-809-42	Sequence 42, Appl
3	20	100.0	20 1 US-09-888-326-463	Sequence 463, Appl
4	20	100.0	20 1 US-09-776-479-311	Sequence 311, Appl
5	20	100.0	20 1 US-10-112-653-301	Sequence 301, Appl
6	20	100.0	20 1 US-10-017-995-311	Sequence 311, Appl
7	17	85.0	20 1 US-10-007-010-56	Sequence 56, Appl
8	13.4	67.0	17 1 US-10-020-038-6	Sequence 6, Appl
9	10	50.0	10 1 US-10-330-627-1410	Sequence 1410, Appl
10	10	50.0	10 1 US-10-330-627-1411	Sequence 1411, Appl
11	10	50.0	12 1 US-09-263-959-437	Sequence 437, Appl
12	9.8	49.0	13 1 US-10-005-212-7	Sequence 7, Appl
13	9	45.0	10 1 US-10-033-145-1619	Sequence 1619, Appl
14	9	45.0	11 1 US-10-055-728-15	Sequence 15, Appl
15	8.8	44.0	12 1 US-09-263-959-437	Sequence 437, Appl
16	8.6	43.0	20 1 US-10-007-010-56	Sequence 56, Appl
17	8.4	42.0	10 1 US-10-329-465-204	Sequence 204, Appl
18	8.4	42.0	10 1 US-10-330-627-420	Sequence 420, Appl
19	8.4	42.0	10 1 US-10-330-627-421	Sequence 421, Appl
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21	8.4	42.0	10 1 US-10-330-627-644	Sequence 644, Appl
22	8.4	42.0	10 1 US-10-330-627-1228	Sequence 1228, Appl
23	8.4	42.0	10 1 US-10-330-627-1229	Sequence 1229, Appl
24	8.4	42.0	10 1 US-10-330-627-1230	Sequence 1230, Appl
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26	8.4	42.0	10 1 US-10-330-627-1232	Sequence 1232, Appl
27	8.4	42.0	10 1 US-10-330-627-1233	Sequence 1233, Appl
28	8.4	42.0	10 1 US-10-330-627-1234	Sequence 1234, Appl
29	8.4	42.0	10 1 US-10-033-145-405	Sequence 405, Appl
30	8.4	42.0	10 1 US-10-033-145-1326	Sequence 1326, Appl
31	8.4	42.0	11 1 US-10-055-728-4	Sequence 4, Appl
32	8	40.0	9 1 US-09-989-789-2374	Sequence 2374, Appl
33	8	40.0	9 1 US-09-989-789-2376	Sequence 2376, Appl

34	8	40.0	9 1 US-09-989-789-2424	Sequence 2424, Appl
35	8	40.0	9 1 US-09-990-186-2374	Sequence 2374, Appl
36	8	40.0	9 1 US-09-990-186-2376	Sequence 2376, Appl
37	8	40.0	9 1 US-09-990-186-2424	Sequence 2424, Appl
38	8	40.0	9 1 US-09-989-994-2374	Sequence 2374, Appl
39	8	40.0	9 1 US-09-989-994-2376	Sequence 2376, Appl
40	8	40.0	9 1 US-09-989-994-2424	Sequence 2424, Appl
41	8	40.0	10 1 US-10-330-627-1228	Sequence 1228, Appl
42	8	40.0	10 1 US-10-330-627-1229	Sequence 1229, Appl
43	8	40.0	10 1 US-10-330-627-1230	Sequence 1230, Appl
44	8	40.0	10 1 US-10-330-627-1231	Sequence 1231, Appl
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48	8	40.0	10 1 US-10-330-627-621	Sequence 621, Appl
49	8	40.0	10 1 US-10-330-627-876	Sequence 876, Appl
50	8	40.0	10 1 US-10-330-627-877	Sequence 877, Appl
51	8	40.0	10 1 US-10-330-627-1214	Sequence 1214, Appl
52	8	40.0	10 1 US-10-330-627-1215	Sequence 1215, Appl
53	8	40.0	10 1 US-10-438-683-6	Sequence 6, Appl
54	8	40.0	10 1 US-10-033-145-62	Sequence 62, Appl
55	8	40.0	10 1 US-10-033-145-1531	Sequence 1531, Appl
56	8	40.0	10 1 US-10-033-145-1750	Sequence 1750, Appl
57	7.8	39.0	11 1 US-10-055-728-15	Sequence 15, Appl
58	7.8	39.0	17 1 US-10-020-038-6	Sequence 6, Appl
59	7.6	38.0	20 1 US-09-774-809-31	Sequence 31, Appl
60	7.6	38.0	20 1 US-09-774-809-42	Sequence 42, Appl
61	7.6	38.0	20 1 US-09-888-326-463	Sequence 463, Appl
62	7.6	38.0	20 1 US-09-776-479-311	Sequence 311, Appl
63	7.6	38.0	20 1 US-10-112-653-301	Sequence 301, Appl
64	7.6	38.0	20 1 US-10-017-995-311	Sequence 311, Appl
65	7.4	37.0	9 1 US-09-989-789-2148	Sequence 2148, Appl
66	7.4	37.0	9 1 US-09-989-789-2149	Sequence 2149, Appl
67	7.4	37.0	9 1 US-09-990-186-2148	Sequence 2148, Appl
68	7.4	37.0	9 1 US-09-990-186-2149	Sequence 2149, Appl
69	7.4	37.0	9 1 US-09-989-994-2148	Sequence 2148, Appl
70	7.4	37.0	9 1 US-09-989-994-2149	Sequence 2149, Appl
71	7.4	37.0	9 1 US-10-277-494-167	Sequence 167, Appl
72	7.4	37.0	10 1 US-10-033-145-405	Sequence 405, Appl
73	7.4	37.0	10 1 US-10-330-627-1214	Sequence 1214, Appl
74	7.4	37.0	10 1 US-10-330-627-1215	Sequence 1215, Appl
75	7	35.0	8 1 US-09-837-751-13	Sequence 13, Appl
76	7	35.0	9 1 US-09-989-789-2396	Sequence 2396, Appl
77	7	35.0	9 1 US-09-989-789-2397	Sequence 2397, Appl
78	7	35.0	9 1 US-09-990-186-2396	Sequence 2396, Appl
79	7	35.0	9 1 US-09-990-186-2397	Sequence 2397, Appl
80	7	35.0	9 1 US-09-989-994-2396	Sequence 2396, Appl
81	7	35.0	9 1 US-09-989-994-2397	Sequence 2397, Appl
82	6.8	34.0	10 1 US-10-330-627-876	Sequence 876, Appl
83	6.8	34.0	10 1 US-10-330-627-877	Sequence 877, Appl
84	6.8	34.0	10 1 US-10-033-145-1750	Sequence 1750, Appl
85	6.4	32.0	8 1 US-10-027-632-176277	Sequence 176277, Appl
86	6.4	32.0	8 1 US-10-027-632-176277	Sequence 176277, Appl

ALIGNMENTS

RESULT 1
US-09-774-809-31
; Sequence 31, Application US/09774809
; Publication No. US20030004120A1
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0412
; CURRENT APPLICATION NUMBER: US/09/774, 809
; CURRENT FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 09/396,902
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 09/130,616
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 08/910,629
PRIOR FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 31
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-774-809-31

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCCAAAGTC 20
DB 1 GTCCGGCCAGGCCAAAGTC 20

RESULT 2

US-09-774-809-42/c
Sequence 42, Application US/09774809
Publication No. US20030004120A1
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0412
CURRENT APPLICATION NUMBER: US/09/774,809
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 09/396,902
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 09/130,616
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 08/910,629
PRIOR FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 42
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-774-809-42

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCCAAAGTC 20
DB 20 GTCCGGCCAGGCCAAAGTC 1

RESULT 3

US-09-888-326-463
Sequence 463, Application US/09888326
Publication No. US20030026801A1
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
FILE REFERENCE: C109/7052 (AWS)

CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 463
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-463

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCCAAAGTC 20
DB 1 GTCCGGCCAGGCCAAAGTC 20

RESULT 4

US-09-776-479-311
Sequence 311, Application US/09776479
Publication No. US20030087848A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 311
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-776-479-311

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCCAAAGTC 20
DB 1 GTCCGGCCAGGCCAAAGTC 20

RESULT 5

US-10-112-653-301
Sequence 301, Application US/10112653
Publication No. US20030050268A1
GENERAL INFORMATION:
APPLICANT: Kriegl, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REFERENCE: C01039/70060 (AWS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642

; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-301

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGGCCAGGCCCAAGTC 20
Db 1 GTCCGGGCCAGGCCCAAGTC 20

RESULT 6
US-10-017-995-311
; Sequence 311, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-311

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCGGGCCAGGCCCAAGTC 20
Db 1 GTCCGGGCCAGGCCCAAGTC 20

RESULT 7
US-10-007-010-56
; Sequence 56, Application US/10007010
; Publication No. US20030125275A1
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
; FILE REFERENCE: RTS-0345
; CURRENT APPLICATION NUMBER: US/10/007,010
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-007-010-56

Query Match 85.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.59;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCGGGCCAGGCCCAAGT 19
Db 4 CCGGGCCAGGCCCAAGT 20

RESULT 8
US-10-020-038-6
; Sequence 6, Application US/10020038
; Publication No. US20020156247A1
; GENERAL INFORMATION:
; APPLICANT: Elledge, Stephen J.
; APPLICANT: Sanchez, Yolanda
; TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
; FILE REFERENCE: 120541-1013
; CURRENT APPLICATION NUMBER: US/10/020,038
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US/09/488,364
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-020-038-6

Query Match 67.0%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.8;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCCAGGCCCAAGTC 20
Db 3 GGACAGGCCCAAGTC 17

RESULT 9
US-10-330-627-1410/C
; Sequence 1410, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1410
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1410

Query Match 50.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCCGGGCCAG 11
Db 10 TCCGGGCCAG 1

RESULT 10
US-10-330-627-1411/C
; Sequence 1411, Application US/10330627

Publication No. US2003017571A1
GENERAL INFORMATION:
APPLICANT: Velculescu, Victor E.
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 09/448,480
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1411
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-330-627-1411

Query Match 50.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCCGGGCCAG 11
Db 10 TCCGGGCCAG 1

RESULT 11
US-09-263-959-437
Sequence 437, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 437:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-437

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGCCA 15
Db 1 GGCCAGGCCA 10

RESULT 12
US-10-005-212-7
Sequence 7, Application US/10005212
Publication No. US20020193570A1
GENERAL INFORMATION:
APPLICANT: GILLIES, Stephen D
APPLICANT: LAN, Yan
APPLICANT: LO, Kin-Ming
TITLE OF INVENTION: Heterodimeric Fusion Proteins Useful for Targeted
FILE REFERENCE: LEX-0020C1
CURRENT APPLICATION NUMBER: US/10/005,212
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: USSN 08/986,997
PRIOR FILING DATE: 1997-12-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-005-212-7

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 16;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGGGCCAGGCCA 15
Db 1 CCGGGCCAGGCCA 13

RESULT 13
US-10-033-145-1619/C
Sequence 1619, Application US/10033145
Publication No. US20020151515A1
GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GA0201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1619
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-145-1619

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AGGCCAAAG 18
Db 10 AGGCCAAAG 2

RESULT 14
US-10-055-728-15/c

Sequence 15, Application US/10055728
Publication No. US20030170720A1
GENERAL INFORMATION:
APPLICANT: van der Kuyt, Antoinette C.
APPLICANT: Cornelissen, Marion
TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
FILE REFERENCE: 5244US (REN/P55190US00)
CURRENT APPLICATION NUMBER: US/10/055,728
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/325,722
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: EP 0120373.2
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: EP 01200228.3
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 11
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: TAG sequence Hs74649
US-10-055-728-15

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCCAGGCC 14
Db 11 GGCCAGGCC 3

RESULT 15
US-09-263-959-437/c
Sequence 437, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 437:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-263-959-437

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGGCGCGGCC 14
Db 12 CTGGCCTGGCC 1

RESULT 16
US-10-007-010-56/c
Sequence 56, Application US/10007010
Publication No. US20030125275A1
GENERAL INFORMATION:
APPLICANT: Alexander H. Borchers
APPLICANT: Kenneth W. Doble
TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
FILE REFERENCE: RTS-0345
CURRENT APPLICATION NUMBER: US/10/007,010
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 56
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-007-010-56

Query Match 43.0%; Score 8.6; DB 1; Length 20;
Best Local Similarity 73.3%; Pred. No. 46;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GGCCAGGCCAAGTC 20
Db 15 GGCCTGGCCCGGCTC 1

RESULT 17
US-10-329-465-204/c
Sequence 204, Application US/10329465
Publication No. US20030165949A1
GENERAL INFORMATION:
APPLICANT: Wang et al.
TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-1
FILE REFERENCE: 27373/37928A
CURRENT APPLICATION NUMBER: US/10/329,465
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 60/343,826
PRIOR FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 315
SOFTWARE: PatentIn version 3.1
SEQ ID NO 204
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-204

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGCCAGGCC 14
Db 10 GTGCCAGGCC 1

RESULT 18

US-10-330-627-420/c
; Sequence 420, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 420
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-420

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCCAGGCCA 15
Db 10 GGCCAGGCCA 1

RESULT 19
US-10-330-627-421/c
; Sequence 421, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 421
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-421

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCCAGGCCA 15
Db 10 GGCCAGGCCA 1

RESULT 20
US-10-330-627-422
; Sequence 422, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30

; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 422
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-422

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GGCCAAAGTC 20
Db 1 GGCCAAAGTC 10

RESULT 21
US-10-330-627-644
; Sequence 644, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 644
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-644

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AGGCCAAGT 19
Db 1 AGGCCAAGT 10

RESULT 22
US-10-330-627-1228/c
; Sequence 1228, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1228
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1228

Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCCAGGCCAA 16
Db 10 GCCTGGCCAA 1

RESULT 23
US-10-330-627-1229/c

; Sequence 1229, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1229
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1229

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCCAGGCCAA 16
Db 10 GCCTGGCCAA 1

RESULT 24
US-10-330-627-1230/c

; Sequence 1230, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1230
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1230

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCCAGGCCAA 16
Db 10 GCCTGGCCAA 1

RESULT 25
US-10-330-627-1231/c
; Sequence 1231, Application US/10330627

; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1231
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1231

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCCAGGCCAA 16
Db 10 GCCTGGCCAA 1

RESULT 26
US-10-330-627-1232/c

; Sequence 1232, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1232
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1232

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCCAGGCCAA 16
Db 10 GCCTGGCCAA 1

RESULT 27
US-10-330-627-1233/c

; Sequence 1233, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1233
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-330-627-1233

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
Db 10 GCCAGGCCAA 1

RESULT 28
US-10-330-627-1234/c
Sequence 1234, Application US/10330627
Publication No. US20030175771A1
GENERAL INFORMATION:
APPLICANT: Velulescu, Victor E.
APPLICANT: Kinzler, Kenneth W
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 09/448,480
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1234
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-330-627-1234

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
Db 10 GCCAGGCCAA 1

RESULT 29
US-10-033-145-405/c
Sequence 405, Application US/10033145
Publication No. US2002015151A1
GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GA0201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: PatentIn version 3.0
SEQ ID NO 405
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-145-405

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCAA 16
Db 10 GCCAGGCCAA 1

RESULT 30
US-10-033-145-1326
Sequence 1326, Application US/10033145
Publication No. US2002015151A1
GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GA0201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1326
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-145-1326

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AGGCCAAAGT 19
Db 1 AGGCCAAAGT 10

RESULT 31
US-10-055-728-4
Sequence 4, Application US/10055728
Publication No. US20030170720A1
GENERAL INFORMATION:
APPLICANT: van der Kuy, Antoinette C.
APPLICANT: Cornelissen, Marion
TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
FILE REFERENCE: 5244US (REN/P55190US00)
CURRENT APPLICATION NUMBER: US/10/055,728
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/325,722
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: EP 0120373.2
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: EP 01200228.3
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 11
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: TAG sequence Hs78436
US-10-055-728-4

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GGCCAAAGTC 20
Db 1 GGCCAAAGTC 10

```
RESULT 32
US-09-989-789-2374/c
; Sequence 2374, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2374
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2374

Query Match
Best Local Similarity 40.0%; Score 8; DB 1; Length 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCCA 15
Db 9 CCAGGCCA 2

RESULT 33
US-09-989-789-2376/c
; Sequence 2376, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2376
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2376

Query Match
Best Local Similarity 40.0%; Score 8; DB 1; Length 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCCA 15
Db 9 CCAGGCCA 2

RESULT 34
US-09-989-789-2424/c
; Sequence 2424, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
```

```
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2424
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2424

Query Match
Best Local Similarity 40.0%; Score 8; DB 1; Length 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCCA 15
Db 9 CCAGGCCA 2

RESULT 35
US-09-990-186-2374/c
; Sequence 2374, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2374
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-2374

Query Match
Best Local Similarity 40.0%; Score 8; DB 1; Length 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCAGGCCA 15
Db 9 CCAGGCCA 2

RESULT 36
US-09-990-186-2376/c
; Sequence 2376, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2376
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-2376
```

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCA 15
| | | | |
Db 9 CCAGGCCA 2

RESULT 37
US-09-990-186-2424/c
; Sequence 2424, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2424
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-2424

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCA 15
| | | | |
Db 9 CCAGGCCA 2

RESULT 38
US-09-989-994-2374/c
; Sequence 2374, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2374
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-2374

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCA 15
| | | | |
Db 9 CCAGGCCA 2

RESULT 39
US-09-989-994-2376/c

; Sequence 2376, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2376
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-2376

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCA 15
| | | | |
Db 9 CCAGGCCA 2

RESULT 40
US-09-989-994-2424/c
; Sequence 2424, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2424
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-2424

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCAGGCCA 15
| | | | |
Db 9 CCAGGCCA 2

RESULT 41
US-10-330-627-1228
; Sequence 1228, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480

;; PRIOR FILING DATE: 1999-11-24
;; NUMBER OF SEQ ID NOS: 1564
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1228
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-330-627-1228

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGC 13
DB 3 GGCCAGGC 10

RESULT 42
US-10-330-627-1229
;; Sequence 1229, Application US/10330627
;; Publication No. US20030175771A1
;; GENERAL INFORMATION:
;; APPLICANT: Velculescu, Victor E.
;; APPLICANT: Kinzler, Kenneth W
;; APPLICANT: Vogelstein, Bert
;; TITLE OF INVENTION: Human Transcriptomes
;; FILE REFERENCE: 001107.00319
;; CURRENT APPLICATION NUMBER: US/10/330,627
;; CURRENT FILING DATE: 2002-12-30
;; PRIOR APPLICATION NUMBER: US 09/448,480
;; PRIOR FILING DATE: 1999-11-24
;; NUMBER OF SEQ ID NOS: 1564
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1229
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-330-627-1229

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGC 13
DB 3 GGCCAGGC 10

RESULT 43
US-10-330-627-1230
;; Sequence 1230, Application US/10330627
;; Publication No. US20030175771A1
;; GENERAL INFORMATION:
;; APPLICANT: Velculescu, Victor E.
;; APPLICANT: Kinzler, Kenneth W
;; APPLICANT: Vogelstein, Bert
;; TITLE OF INVENTION: Human Transcriptomes
;; FILE REFERENCE: 001107.00319
;; CURRENT APPLICATION NUMBER: US/10/330,627
;; CURRENT FILING DATE: 2002-12-30
;; PRIOR APPLICATION NUMBER: US 09/448,480
;; PRIOR FILING DATE: 1999-11-24
;; NUMBER OF SEQ ID NOS: 1564
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1230
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-330-627-1230

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GGCCAGGC 13
DB 3 GGCCAGGC 10

RESULT 44
US-10-330-627-1231
;; Sequence 1231, Application US/10330627
;; Publication No. US20030175771A1
;; GENERAL INFORMATION:
;; APPLICANT: Velculescu, Victor E.
;; APPLICANT: Kinzler, Kenneth W
;; APPLICANT: Vogelstein, Bert
;; TITLE OF INVENTION: Human Transcriptomes
;; FILE REFERENCE: 001107.00319
;; CURRENT APPLICATION NUMBER: US/10/330,627
;; CURRENT FILING DATE: 2002-12-30
;; PRIOR APPLICATION NUMBER: US 09/448,480
;; PRIOR FILING DATE: 1999-11-24
;; NUMBER OF SEQ ID NOS: 1564
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1231
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-330-627-1231

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGC 13
DB 3 GGCCAGGC 10

RESULT 45
US-10-330-627-1232
;; Sequence 1232, Application US/10330627
;; Publication No. US20030175771A1
;; GENERAL INFORMATION:
;; APPLICANT: Velculescu, Victor E.
;; APPLICANT: Kinzler, Kenneth W
;; APPLICANT: Vogelstein, Bert
;; TITLE OF INVENTION: Human Transcriptomes
;; FILE REFERENCE: 001107.00319
;; CURRENT APPLICATION NUMBER: US/10/330,627
;; CURRENT FILING DATE: 2002-12-30
;; PRIOR APPLICATION NUMBER: US 09/448,480
;; PRIOR FILING DATE: 1999-11-24
;; NUMBER OF SEQ ID NOS: 1564
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1232
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-330-627-1232

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCAGGC 13
DB 3 GGCCAGGC 10

RESULT 46
US-10-330-627-1233
;; Sequence 1233, Application US/10330627
;; Publication No. US20030175771A1

```
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1233
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1233

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCAGGC 13
Db 3 GGGCAGGC 10

RESULT 47
US-10-330-627-1234
; Sequence 1234, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1234
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1234

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGCAGGC 13
Db 3 GGGCAGGC 10

RESULT 48
US-10-330-627-621
; Sequence 621, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1564
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1564
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 621
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-621

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCCAGG 12
Db 1 GGGCCAGG 8

RESULT 49
US-10-330-627-876/C
; Sequence 876, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 876
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-876

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCCAGGCC 14
Db 10 GCCAGGCC 3

RESULT 50
US-10-330-627-877/C
; Sequence 877, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 877
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-877

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 7 GCCAGGCC 14
 |||||
 Db 10 GCCAGGCC 3

RESULT 51

US-10-330-627-1214/C
 ; Sequence 1214, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcripts
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1214
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-330-627-1214

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCAGGCC 13
 |||||
 Db 8 GCCAGGCC 1

RESULT 52

US-10-330-627-1215/C
 ; Sequence 1215, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcripts
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1215
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-330-627-1215

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCAGGCC 13
 |||||
 Db 8 GCCAGGCC 1

RESULT 53
 US-10-438-683-6/C
 ; Sequence 6, Application US/10438683
 ; Publication No. US20030186923A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JAMES D. THOMPSON

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TITLE OF INVENTION: METHOD AND REAGENT FOR
 INHIBITING P-GLYCOPROTEIN mdr-
 1 GENE

NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 611 West Sixth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90017

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 COMPUTER: IBM COMPATIBLE
 OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/438,683
 FILING DATE: 15-May-2003
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/882,885
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,337
 REFERENCE/DOCKET NUMBER: 197/173
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 ; US-10-438-683-6

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCAAGT 19
 |||||
 Db 10 GCCAAGT 3

RESULT 54

US-10-033-145-62/C
 ; Sequence 62, Application US/10033145
 ; Publication No. US20020151515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 62
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-033-145-62

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CAGGCCCA 16
| | | | |
Db 10 CAGGCCCA 3

RESULT 55
US-10-033-145-1531/c
; Sequence 1531, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: CA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1531
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1531

Query Match
Best Local Similarity 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCAAGTC 20
| | | | |
Db 8 CCAAGTC 1

RESULT 56
US-10-033-145-1750/c
; Sequence 1750, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: CA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1750
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1750

Query Match
Best Local Similarity 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCCAGGCC 14
| | | | |
Db 10 GCCAGGCC 3

RESULT 57
US-10-055-728-15
; Sequence 15, Application US/10055728
; Publication No. US20030170720A1

; GENERAL INFORMATION:
; APPLICANT: van der Kuyt, Antoinette C.
; APPLICANT: Corneliussen, Marion
; TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
; FILE REFERENCE: 5244US (REN/P55190US00)
; CURRENT APPLICATION NUMBER: US/10/055,728
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,722
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 0120373.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TAG sequence Hs74649
US-10-055-728-15

Query Match
Best Local Similarity 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 32;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGGCCAGGCC 14
| | | | |
Db 1 CGGCCAGGCC 11

RESULT 58
US-10-020-038-6/c
; Sequence 6, Application US/10020038
; Publication No. US20020156247A1
; GENERAL INFORMATION:
; APPLICANT: Elledge, Stephen J.
; APPLICANT: Sanchez, Yolanda
; TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
; FILE REFERENCE: 120541-1013
; CURRENT APPLICATION NUMBER: US/10/020,038
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US/09/488,364
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-020-038-6

Query Match
Best Local Similarity 39.0%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCAGGCCAA 16
| | | | |
Db 11 GGCAGGCCAA 1

RESULT 59
US-09-774-809-31/c
; Sequence 31, Application US/09774809
; Publication No. US20030004120A1
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam

APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0412
CURRENT APPLICATION NUMBER: US/09/774,809
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 09/396,902
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 09/130,616
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 08/910,629
PRIOR FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 31
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-774-809-31

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGGCCAGGCC 14
DB 14 GGCCTGGCCCGGAC 1

RESULT 60

US-09-774-809-42
Sequence 42, Application US/09774809
Publication No. US20030004120A1
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monta, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0412
CURRENT APPLICATION NUMBER: US/09/774,809
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 09/396,902
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 09/130,616
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 08/910,629
PRIOR FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 42
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-774-809-42

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGGCCAGGCC 14
DB 7 GGCCTGGCCCGGAC 20

RESULT 61
US-09-888-326-463/C
Sequence 463, Application US/09888326
Publication No. US20030026801A1

GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
FILE REFERENCE: C1039/7052 (AMS)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,146
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 463
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc_feature
LOCATION: (0)..(0)
OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-463

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGGCCAGGCC 14
DB 14 GGCCTGGCCCGGAC 1

RESULT 62
US-09-776-479-311/C
Sequence 311, Application US/09776479
Publication No. US20030087848A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouyon, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 311
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-776-479-311

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGGCCAGGCC 14
DB 14 GGCCTGGCCCGGAC 1

RESULT 63
US-10-112-653-301/C
Sequence 301, Application US/10112653
Publication No. US20030050268A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REFERENCE: C01039/70060 (AMS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 301
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-301

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCC 14
DB 14 GGCTGTGCGCCGAC 1

RESULT 64
US-10-017-995-311/C
Sequence 311, Application US/10017995
Publication No. US20030055014A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
FILE REFERENCE: C1037/7025 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/255,534
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 311
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-017-995-311

Query Match 38.0%; Score 7.6; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCCGGCCAGGCC 14
DB 14 GGCTGTGCGCCGAC 1

RESULT 65
US-09-989-789-2148
Sequence 2148, Application US/09989789
Patent No. US20020063379A1
GENERAL INFORMATION:
APPLICANT: Liu, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2148
LENGTH: 9
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2148

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGC 13
DB 1 GGGCCAGGC 9

RESULT 66
US-09-989-789-2149
Sequence 2149, Application US/09989789
Patent No. US20020063379A1
GENERAL INFORMATION:
APPLICANT: Liu, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2149
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2149

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGC 13
DB 1 GGGCCAGGC 9

RESULT 67
US-09-990-186-2148
Sequence 2148, Application US/09990186
Publication No. US20030068675A1
GENERAL INFORMATION:
APPLICANT: Liu, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2148
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-2148

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGC 13

Db 1 GGGGCGAGC 9

RESULT 68
US-09-990-186-2149
; Sequence 2149, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIT, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2149
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-2149

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCGAGC 13
Db 1 GGGGCGAGC 9

RESULT 69
US-09-989-994-2148
; Sequence 2148, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIT, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2148
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-2148

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCGAGC 13
Db 1 GGGGCGAGC 9

RESULT 70
US-09-989-994-2149
; Sequence 2149, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIT, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2149
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-2149

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCGAGC 13
Db 1 GGGGCGAGC 9

RESULT 71
US-10-277-494-167
; Sequence 167, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related To Leve
; FILE REFERENCE: MEH00-958-X (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 167
; LENGTH: 9
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-277-494-167

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGGCGAGC 11
Db 1 CUGGCGAGC 9

RESULT 72
US-10-033-145-405
; Sequence 405, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKAR, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 405
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-033-145-405

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCCAGGC 13
|||
Db 2 GGGCCTGGC 10

RESULT 73

US-10-330-627-1214
; Sequence 1214, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1214
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1214

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCA 15
|||
Db 1 GCCTGGCCA 9

RESULT 74
US-10-330-627-1215
; Sequence 1215, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1215
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1215

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCCAGGCCA 15
|||
Db 1 GCCTGGCCA 9

RESULT 75

US-09-837-751-13/c
; Sequence 13, Application US/09837751
; Patent No. US20020104124A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Liu, Qing
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
; FILE REFERENCE: 45-00
; CURRENT APPLICATION NUMBER: US/09/837,751
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,124
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide useful as a primer
US-09-837-751-13

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGGGCC 9
|||
Db 7 CCGGGCC 1

RESULT 76
US-09-989-789-2396/c
; Sequence 2396, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2396
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2396

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCAAG 18
|||
Db 8 GCCAAG 2

RESULT 77
US-09-989-789-2397/c
; Sequence 2397, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
US-09-989-789-2397


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FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2397
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2397

Query Match
Best Local Similarity 35.0%; Score 7; DB 1; Length 9;
Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCAAG 18
DB 8 GCCAAG 2

RESULT 78
US-09-990-186-2396/c
Sequence 2396, Application US/09990186
Publication No. US20030068675A1
GENERAL INFORMATION:
APPLICANT: Liu, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2396
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-2396

Query Match
Best Local Similarity 35.0%; Score 7; DB 1; Length 9;
Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCAAG 18
DB 8 GCCAAG 2

RESULT 79
US-09-990-186-2397/c
Sequence 2397, Application US/09990186
Publication No. US20030068675A1
GENERAL INFORMATION:
APPLICANT: Liu, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2397
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
```

```
OTHER INFORMATION: DNA
US-09-990-186-2397

Query Match
Best Local Similarity 35.0%; Score 7; DB 1; Length 9;
Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCAAG 18
DB 8 GCCAAG 2

RESULT 80
US-09-989-994-2396/c
Sequence 2396, Application US/09989994
Publication No. US20030104526A1
GENERAL INFORMATION:
APPLICANT: Liu, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,994
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2396
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-2396

Query Match
Best Local Similarity 35.0%; Score 7; DB 1; Length 9;
Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCAAG 18
DB 8 GCCAAG 2

RESULT 81
US-09-989-994-2397/c
Sequence 2397, Application US/09989994
Publication No. US20030104526A1
GENERAL INFORMATION:
APPLICANT: Liu, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,994
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2397
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-2397

Query Match
Best Local Similarity 35.0%; Score 7; DB 1; Length 9;
Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCAAG 18
DB 8 GCCAAG 2
```

RESULT 82
US-10-330-627-876
; Sequence 876, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcription
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 876
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-876

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGGGCCAGGC 13
| | | | |
Db 1 CAGGCTGGC 10

RESULT 83
US-10-330-627-877
; Sequence 877, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcription
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 877
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-877

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGGGCCAGGC 13
| | | | |
Db 1 CAGGCTGGC 10

RESULT 84
US-10-033-145-1750
; Sequence 1750, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: G40201C

; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1750
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1750

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGGGCCAGGC 13
| | | | |
Db 1 CAGGCTGGC 10

RESULT 85
US-10-027-632-176277
; Sequence 176277, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176277
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176277

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1,2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCAGCCCA 15
| | | | |
Db 1 CCAGCCCA 8

RESULT 86
US-10-027-632-176277
; Sequence 176277, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30

```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176277
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176277

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Query Match      32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCAGGCCA 15
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Db       1 CCAGGCCA 8

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Search completed: November 10, 2003, 08:06:57
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2003, 08:08:11 ; Search time 0.001 Seconds
(without alignments)
0.320 Million cell updates/sec

Title: us-09-774-809-31
Perfect score: 20
Sequence: 1 gtccggccagcccaagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 8 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database: rst.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	6	30.0	8	1	CD486474
2	2.4	12.0	8	1	CD486474

ACCESSION: CD486474
ACCESSION: CD486474

ALIGNMENTS

RESULT 1
CD486474/c
LOCUS
DEFINITION
CD486474 8 bp mRNA linear EST 04-JUN-2003
CD486474
CD486474
CD486474.1 GI:31407439
EST.
Gossypium hirsutum (upland cotton)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eucosids II; Malvales; Malvaceae; Malvaceae; Gossypium.
1 (bases 1 to 8)
Dowd, C., Wilson, I. and McFadden, H.
Different Gene Expression Responses in Cotton Root and Hypocotyl tissues during infection with Fusarium Wilt Disease
Unpublished (2003)
Contact: Caitriona Dowd, Helen McFadden
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Black Mountain Laboratories, Cnr Clunies Ross Street & Barry Drive, Black Mountain, Canberra, ACT, 2601, Australia
Tel: 61 2 6246 4914, 6246 5377
Fax: 61 2 6246 5000
Email: Caitriona.Dowd@csiro.au, Helen.McFadden@csiro.au

Vector clipped sequences Bases 1-17 (GTGACCCAGCGTCG) : Sali adapter
Seq primer: M13 reverse primer
High quality sequence stop: 8.
Location/Qualifiers
1. 8
/organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultiar="DeltaEMERALD"
/db_xref="taxon:3635"
/clone="CRH2.4F08"
/tissue_type="Root and hypocotyl tissues"
/dev_stage="5 day old seedlings"
/lab_host="Y1090(ZL)"
/clone_lib="Cotton Root and Hypocotyl Lambda ZIPLOX Library (CRH)"
/note="Vector: Lambda ZIPLOX; Site 1: Sali; Site 2: NotI; mRNA was prepared from root and hypocotyl tissues of the cotton cultivar DeltaEMERALD. cDNA was synthesised from a NotI-oligodT primer/adaptor using the manufacturers protocols (Life Technologies) and then ligated to a Sali adapter to facilitate directional cloning. The cDNA was cloned into the Sali and NotI sites of the Lambda ZIPLOX phage vector (Life Technologies). Constructed by Caitriona Dowd and Helen McFadden."

BASE COUNT
3 a 1 c 1 g 3 t
Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CAAAGT 19
Db 7 CAAAGT 2

RESULT 2
CD486474
LOCUS
DEFINITION
CD486474 8 bp mRNA linear EST 04-JUN-2003
CD486474
CD486474
CD486474.1 GI:31407439
EST.
Gossypium hirsutum (upland cotton)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eucosids II; Malvales; Malvaceae; Malvaceae; Gossypium.
1 (bases 1 to 8)
Dowd, C., Wilson, I. and McFadden, H.
Different Gene Expression Responses in Cotton Root and Hypocotyl tissues during infection with Fusarium Wilt Disease
Unpublished (2003)
Contact: Caitriona Dowd, Helen McFadden
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Black Mountain Laboratories, Cnr Clunies Ross Street & Barry Drive, Black Mountain, Canberra, ACT, 2601, Australia
Tel: 61 2 6246 4914, 6246 5377
Fax: 61 2 6246 5000
Email: Caitriona.Dowd@csiro.au, Helen.McFadden@csiro.au
Vector clipped sequences Bases 1-17 (GTGACCCAGCGTCG) : Sali adapter
Seq primer: M13 reverse primer
High quality sequence stop: 8.
Location/Qualifiers
1. 8
/organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultiar="DeltaEMERALD"
/db_xref="taxon:3635"
/clone="CRH2.4F08"

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/tissue type="Root and hypocotyl tissues"
/dev stage="5 day old seedlings"
/lab_host="Y1090(ZL)"
/clone_lib="Cotton Root and Hypocotyl Lambda ZIPLOX
Library (CRH)"
/note="Vector: Lambda ZIPLOX; Site_1: SalI; Site_2: NotI;
mRNA was prepared from root and hypocotyl tissues of the
cotton cultivar DeltaEMERALD. cDNA was synthesised from a
NotI-oligodT primer/adaptor using the manufacturers
protocols (Life Technologies) and then ligated to a SalI
adaptor to facilitate directional cloning. The cDNA was
cloned into the SalI and NotI sites of the Lambda ZIPLOX
phage vector (Life Technologies). Constructed by California
Dowd and Helen McFadden."
BASE COUNT      3 a      1 c      1 g      3 t
Query Match      12.0%; Score 2.4; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      16 AGT 19
Db      1 AACT 4

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Search completed: November 10, 2003, 08:08:11
 Job time : 0.001 secs